09701586 09/701586

529 Rec'd PCT/PTO 30 NOV 2000

TRANSMITTAL LETTER TO THE UNITED STATES ATTORNEY'S DOCKET NUMBER 49100

DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371 U.S. APPLICATION NO. (If known, see 37 CFR 1.5)

INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/EP 99/03889	**4 June 1999**	**5 June 1998** 1 March 1999

TITLE OF INVENTION: POLY(ADP-RIBOSE)POLYMERASE-GENE

APPLICANT(S) FOR DO/EO/US Michael KOCK, Thomas HOEGER, Burkhard KROEGER, Bernd OTTERBACH Wilfried LUBISCH, Hans-Georg LEMAIRE

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. /X/ This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.

2. / / This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.

3. /X/ This express request to begin national examination procedures (35 U.S.C.371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).

4. /x/ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.

5. /X/ A copy of the International Application as filed (35 U.S.C. 371(c)(2)).

   a./X/ is transmitted herewith (required only if not transmitted by the International Bureau).
   b./ / has been transmitted by the International Bureau.
   c./ / is not required, as the application was filed in the United States Receiving Office (RO/US0).

6. /X/ A translation of the International Application into English (35 U.S.C. 371(c)(2)).

7. /X/ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)).

   a./X/ are transmitted herewith (required only if not transmitted by the International Bureau).
   b./ / have been transmitted by the International Bureau.
   c./ / have not been made; however, the time limit for making such amendments has NOT expired.
   d./ / have not been made and will not be made.

8. /X/ A translation of the amendments to the claims under PCT Article 19(35 U.S.C. 371(c)(3)).

9. /X/ An oath or declaration of the inventor(s)(35 U.S.C. 171(c)(4)).

10./ / A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern other document(s) or information included:

11./ / An Information Disclosure Statement under 37 CFR 1.97 and 1.98.

12./X/ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.

13./X/ A FIRST preliminary amendment.
/ / A SECOND or SUBSEQUENT preliminary amendment.

14./ / A substitute specification.

15./ / A change of power of attorney and/or address letter.

16./x/ Other items or information.
International Search Report
International Preliminary Examination Report

09/701586 JC13 Rec'd PCT/PTO 30 NOV 2000

U.S. Appln. No. (If Known)	INTERNATIONAL APPLN. NO.	ATTORNEY'S DOCKET NO.
09/701586	PCT/EP99/03889	49790

17. /X/ The following fees are submitted

	CALCULATIONS	PTO USE ONLY
BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)): Search Report has been prepared by the EPO or JPO.....$860.00	860.00	
International preliminary examination fee paid to USPTO (37 CFR 1.482).....$750.00		
No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)).....$700.00		
Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO .....$ 970.00		
International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied pro -visions of PCT Article 33(2)-(4).....$96.00		
ENTER APPROPRIATE BASIC FEE AMOUNT =	$ 860.00	
Surcharge of $130.00 for furnishing the oath or declaration later than / / 20 / /30 months from the earliest claimed priority date (37 CFR 1.492(e)).		

Claims	Number Filed		Number Extra	Rate	
					216.00
Total Claims	32	-20	12	X$18.	
Indep.Claims	1	-3		X$80.	
Multiple dependent claim(s)(if applicable)			+270.		
TOTAL OF ABOVE CALCULATION				=	**1,076.00**
Reduction of 1/2 for filing by small entity, if applicable. Verified Small Entity statement must also be filed (Note 37 CFR 1.9, 1.27, 1.28).					
SUBTOTAL				=	1,076.00
Processing fee of $130. for furnishing the English translation later than / /20 / /30 months from the earliest claimed priority date (37 CFR 1.492(f)).				+	
TOTAL NATIONAL FEE				=	**1,076.00**
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31) $40.00 per property				=	40.00
TOTAL FEES ENCLOSED				=	**$ 1,116.00**
				Amount to be refunded:	$
				Charged	$

a./X/ A check in the amount of $ 1,116.00. to cover the above fees is enclosed.

b./ / Please charge my Deposit Account No._____ in the amount of $_____ to cover the above fees. A duplicate copy of this sheet is enclosed.

c./X/ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. **11-0345**. A duplicate copy of this sheetis enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:
KEIL & WEINKAUF
1101 Connecticut Ave., N.W.
Washington, D. C. 20036

Herbert B Keil
SIGNATURE

Herbert B. Keil
NAME
Registration No. 18,967

#8 Box Sequence

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of)
)
KOCK et al.)
)
Serial No. 09/701,586)
)
Filed: November 30, 2000)
)
For: POLY(ADP-RIBOSE) POLYMERASE-GENE

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner of Patents and Trademarks, Washington, D C 20231, on April 23, 2002

Date of Deposit

Herbert B. Keil

Person Making Deposit

Signature

April 23, 2002

Date of Signature

Honorable Commissioner of
Patents and Trademarks
Washington, D.C. 20231

PRELIMINARY AMENDMENT
AND
RESPONSE TO NOTIFICATION OF DEFECTIVE RESPONSE

Sir:

In response to the Notification of Defective Response, mailed April 11, 2002, applicants respectfully request entry of the following amendments, in accordance with 37 CFR §1.115.

CLEAN VERSION OF AMENDMENTS

IN THE SPECIFICATION

Please replace the sequence listing on pages 48 to 82 of the specification with the substitute sequence listing appended hereto, numbered pages 1 to 36.

REMARKS

In response to the Notice of Defective Response, a copy of the substitute sequence listing in computer readable form is attached hereto. The content of the paper copy of the sequence listing and the copy of the sequence listing in computer readable form is the same, and includes no new matter.

It is believed that by submitting the present amendment and the sequence listing diskette, the application now fully complies with the requirements of 37 CFR §§ 1.821-1.825. Applicants respectfully solicit issuance of the patent.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such deposit account.

Respectfully submitted,
KEIL & WEINKAUF

David C. Liechty
Reg. No. 48,692

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Washington, D.C. 20036
(202)659-0100

DCL/kas

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of)
KOCK et al.) BOX PCT
)
International Application)
PCT/EP 99/03889)
)
Filed: June 4, 1999)
)
For: POLY(ADP-RIBOSE)POLYMERASE-GENE

PRELIMINARY AMENDMENT

Honorable Commissioner of
Patents and Trademarks
Washington, D.C. 20231

Sir:

Prior to examination, kindly amend the above-identified application as follows:

IN THE CLAIMS

3. A PARP homolog as claimed in claim 1 [either of the preceding claims], comprising at least another one of the following part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$,
$AX_3FXKX_4KTXNXWX_5FX_3PXK$,
$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$,
FYTXIPHXFGX_3PP; and
$KX_3LX_2LXDIEXAX_2L$,

in which the X radicals are, independently of one another, any amino acid.

4. A PARP homolog as claimed in claim 1 [any of the preceding claims], selected from human PARP homologs, which has the amino acid sequence shown in SEQ ID NO: 2 (human PARP2) or SEQ ID NO: 4 or 6 (human PARP3 type 1 or 2); or murine PARP homologs which have the amino acid sequence shown in SEQ ID NO:8 (mouse PARP long form) or SEQ ID No:10 (mouse PARP short form); and the functional equivalents thereof.

5. A binding partner for PARP homologs as claimed in claim 1 [any of the preceding claims], selected from

a) antibodies and fragments thereof,

b) protein-like compounds which interact with a part-sequence of the protein, and

c) low molecular weight effectors which modulate the catalytic PARP activity or another biological function of a PARP molecule.

6. A nucleic acid comprising

a) a nucleotide sequence coding for at least one PARP homolog as claimed in claim 1 [any of claims 1 to 4], or the complementary nucleotide sequence thereof;

b) a nucleotide sequence which hybridizes with a sequence as specified in a) under stringent conditions; or

c) nucleotide sequences which are derived from the nucleotide sequences defined in a) and b) through the degeneracy of the genetic code.

8. An expression cassette comprising, under the genetic control of at least one regulatory nucleotide sequence, at least one nucleotide sequence as claimed in claim 6 [either of claims 6 and 7].

12. A PARP-deficient mammal or PARP-deficient eukaryotic cell, in which functional expression of at least one gene which codes for a PARP homolog as claimed in claim 1 [any of claims 1 to 4] is inhibited.

13. An in vitro detection method for PARP inhibitors, which comprises

a) incubating an unsupported or supported polyADP-ribosylatable target with a reaction mixture comprising
   - a1) a PARP homolog as claimed in claim 1 [any of claims 1 to 4],
   - a2) a PARP activator; and
   - a3) a PARP inhibitor or an analyte in which at least one PARP inhibitor is suspected;

b) carrying out the polyADP ribosylation reaction; and

c) determining the polyADP ribosylation of the target qualitatively or quantitatively.

15. A method as claimed in claim 13 [either of claims 13 and 14], wherein the polyADP-ribosylatable target is a histone protein.

16. A method as claimed in claim 13 [any of claims 13 to 15], wherein the PARP activator is activated DNA.

17. A method as claimed in claim 13 [any of claims 13 to 16], wherein the polyADP ribosylation reaction is started by adding NAD^+.

18. A method as claimed in claim 13 [any of claims 13 to 17], wherein the polyADP ribosylation of the supported target is determined using anti-poly(ADP-ribose) antibodies.

19. A method as claimed in claim 13 [any of claims 13 to 17], wherein the unsupported target is labeled with an acceptor fluorophore.

21. A method as claimed in claim 19 [either of claims 19 and 20], wherein the target is biotinylated histone, and the acceptor fluorophore is coupled thereto via avidin or streptavidin.

22. A method as claimed in claim 20 [either of claims 20 and 21], wherein the anti-poly(ADP-ribose) antibody carries a europium cryptate as donor fluorophore.

23. An in vitro screening method for binding partners for a PARP molecule, which comprises

a1) immobilizing at least one PARP homolog as claimed in claim 1 [any of claims 1 to 4] on a support;

b1) contacting the immobilized PARP homolog with an analyte in which at least one binding partner is suspected; and

c1) determining, where appropriate after an incubation period, analyte constituents bound to the immobilized PARP homolog;

or

a2) immobilizing on a support an analyte which comprises at least one possible binding partner for a PARP molecule;
b2) contacting the immobilized analyte with at least one PARP homolog as claimed in claim 1 [any of claims 1 to 4] for which a binding partner is sought; and
c2) examining the immobilized analyte, where appropriate after an incubation period, for binding of the PARP homolog.

24. A method for the qualitative or quantitative determination of nucleic acids encoding a PARP homolog as claimed in claim 1 [any of claims 1 to 4], which comprises
a) incubating a biological sample with a defined amount of an exogenous nucleic acid [as claimed in either of claims 6 and 7], hybridizing under stringent conditions, determining the hybridizing nucleic acids and, where appropriate, comparing with a standard; or

b) incubating a biological sample with a pair of oligonucleotide primers with specificity for a PARP homolog-encoding nucleic acid, amplifying the nucleic acid, determining the amplification product and, where appropriate, comparing with a standard.

25. A method for the qualitative or quantitative determination of a PARP homolog as claimed in claim 1 [any of claims 1 to 4], which comprises
a) incubating a biological sample with a binding partner specific for a

PARP homolog,

b) detecting the binding partner/PARP complex and, where appropriate,

c) comparing the result with a standard.

27. A method as claimed in claim 24 [any of claims 24 to 26] for diagnosing energy deficit-mediated illnesses.

28. A method for determining the efficacy of PARP effectors, which comprises

a) incubating a PARP homolog as claimed in claim 1 [any of claims 1 to 4] with an analyte which comprises an effector of a physiological or pathological PARP activity; removing the effector again where appropriate; and

b) determining the activity of the PARP homolog, where appropriate after adding substrates or cosubstrates.

29. A gene therapy composition, which comprises in a vehicle acceptable for gene therapy a nucleic acid construct which

a) comprises an antisense nucleic acid against a coding nucleic acid as claimed in claim 6 [either of claims 6 and 7]; or

b) a ribozyme against a nucleic acid as claimed in claim 6 [either of claims 6 and 7]; or

c) codes for a specific PARP inhibitor.

30. A pharmaceutical composition comprising, in a pharmaceutically acceptable vehicle, at least one PARP protein as claimed in claim 1 [any of claims 1 to 4], at least one PARP binding partner [as claimed in claim 5] or at least one coding nucleotide sequence [as claimed in claim 6 or 7].

REMARKS

The claims have been amended to eliminate multiple dependency and to put them in better form for U.S. filing. No new matter is included. A clean copy of the claims is attached.

Favorable action is solicited.

Respectfully submitted,

KEIL & WEINKAUF

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(202)659-0100

10050/49100/49790

CLEAN COPY OF THE CLAIMS

1. A poly(ADP-ribose) polymerase (PARP) homolog which has an amino acid sequence which has
   a) a functional NAD^+ binding domain
      and
   b) no zinc finger sequence motif of the general formula

$$CX_2CX_mHX_2C$$

in which
m is an integral value from 28 or 30, and the X radicals are,
independently of one another, any amino acid;
and the functional equivalents thereof.

2. A PARP homolog as claimed in claim 1, wherein the functional NAD^+ binding domain comprises one of the following general sequence motifs:

$PX_n(S/T)GX_3GKGIYFA$,
$(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFA$ or
$LLWHG(S/T)X_7IL(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFAX_3SKSAXY$

in which
n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid.

3. A PARP homolog as claimed in claim 1, comprising at least another one of the following part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$,
$AX_3FXKX_4KTXNXWX_5FX_3PXK$,

$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$,
$FYTXIPHXFGX_3PP$; and
$KX_3LX_2LXDIEXAX_2L$,

in which the X radicals are, independently of one another, any amino acid.

4. A PARP homolog as claimed in claim 1, selected from human PARP homologs, which has the amino acid sequence shown in SEQ ID NO: 2 (human PARP2) or SEQ ID NO: 4 or 6 (human PARP3 type 1 or 2); or murine PARP homologs which have the amino acid sequence shown in SEQ ID NO:8 (mouse PARP long form) or SEQ ID No:10 (mouse PARP short form); and the functional equivalents thereof.

5. A binding partner for PARP homologs as claimed in claim 1, selected from
   a) antibodies and fragments thereof,
   b) protein-like compounds which interact with a part-sequence of the protein, and
   c) low molecular weight effectors which modulate the catalytic PARP activity or another biological function of a PARP molecule.

6. A nucleic acid comprising
   a) a nucleotide sequence coding for at least one PARP homolog as claimed in claim 1, or the complementary nucleotide sequence thereof;
   b) a nucleotide sequence which hybridizes with a sequence as specified in a) under stringent conditions; or
   c) nucleotide sequences which are derived from the nucleotide sequences defined in a) and b) through the degeneracy of the genetic code.

7. A nucleic acid as claimed in claim 6, comprising

   a) nucleotides +3 to +1715 shown in SEQ ID NO:1;

b) nucleotides +242 to +1843 shown in SEQ ID NO:3;
c) nucleotides +221 to +1843 shown in SEQ ID NO:5;
d) nucleotides +112 to +1710 shown in SEQ ID NO:7; or
e) nucleotides +1 to +1584 shown in SEQ ID NO:9.

8. An expression cassette comprising, under the genetic control of at least one regulatory nucleotide sequence, at least one nucleotide sequence as claimed in claim 6.

9. A recombinant vector comprising at least one expression cassette as claimed in claim 8.

10. A recombinant microorganism comprising at least one recombinant vector as claimed in claim 9.

11. A transgenic mammal comprising a vector as claimed in claim 9.

12. A PARP-deficient mammal or PARP-deficient eukaryotic cell, in which functional expression of at least one gene which codes for a PARP homolog as claimed in claim 1 is inhibited.

13. An in vitro detection method for PARP inhibitors, which comprises

a) incubating an unsupported or supported polyADP-ribosylatable target with a reaction mixture comprising
   a1) a PARP homolog as claimed in claim 1,
   a2) a PARP activator; and
   a3) a PARP inhibitor or an analyte in which at least one PARP inhibitor is suspected;
b) carrying out the polyADP ribosylation reaction; and
c) determining the polyADP ribosylation of the target qualitatively or

quantitatively.

14. A method as claimed in claim 13, wherein the PARP homolog is preincubated with the PARP activator and the PARP inhibitor or an analyte in which at least one PARP inhibitor is suspected, before the polyADP ribosylation reaction is carried out.

15. A method as claimed in claim 13, wherein the polyADP-ribosylatable target is a histone protein.

16. A method as claimed in claim 13, wherein the PARP activator is activated DNA.

17. A method as claimed in claim 13, wherein the polyADP ribosylation reaction is started by adding NAD^+.

18. A method as claimed in claim 13, wherein the polyADP ribosylation of the supported target is determined using anti-poly(ADP-ribose) antibodies.

19. A method as claimed in claim 13, wherein the unsupported target is labeled with an acceptor fluorophore.

20. A method as claimed in claim 19, wherein the polyADP ribosylation of the unsupported target is determined using anti-poly(ADP-ribose) antibody which is labeled with a donor fluorophore which is able to transfer energy to the acceptor fluorophore.

21. A method as claimed in claim 19, wherein the target is biotinylated histone, and the acceptor fluorophore is coupled thereto via avidin or streptavidin.

22. A method as claimed in claim 20, wherein the anti-poly(ADP-ribose) antibody

carries a europium cryptate as donor fluorophore.

23. An in vitro screening method for binding partners for a PARP molecule, which comprises

a1) immobilizing at least one PARP homolog as claimed in claim 1 on a support;

b1) contacting the immobilized PARP homolog with an analyte in which at least one binding partner is suspected; and

c1) determining, where appropriate after an incubation period, analyte constituents bound to the immobilized PARP homolog;

or

a2) immobilizing on a support an analyte which comprises at least one possible binding partner for a PARP molecule;

b2) contacting the immobilized analyte with at least one PARP homolog for which a binding partner is sought; and

c2) examining the immobilized analyte, where appropriate after an incubation period, for binding of the PARP homolog.

24. A method for the qualitative or quantitative determination of nucleic acids encoding a PARP homolog as claimed in claim 1, which comprises

a) incubating a biological sample with a defined amount of an exogenous nucleic acid, hybridizing under stringent conditions, determining the hybridizing nucleic acids and, where appropriate, comparing with a standard; or

b) incubating a biological sample with a pair of oligonucleotide primers with specificity for a PARP homolog-encoding nucleic acid, amplifying the nucleic acid, determining the amplification product and, where appropriate, comparing with a standard.

25. A method for the qualitative or quantitative determination of a PARP homolog as claimed in claim 1, which comprises
    a) incubating a biological sample with a binding partner specific for a PARP homolog,
    b) detecting the binding partner/PARP complex and, where appropriate,
    c) comparing the result with a standard.

26. A method as claimed in claim 25, wherein the binding partner is an antibody or a binding fragment thereof, which carries a detectable label where appropriate.

27. A method as claimed in claim 24 for diagnosing energy deficit-mediated illnesses.

28. A method for determining the efficacy of PARP effectors, which comprises
    a) incubating a PARP homolog as claimed in claim 1 with an analyte which comprises an effector of a physiological or pathological PARP activity; removing the effector again where appropriate; and
    b) determining the activity of the PARP homolog, where appropriate after adding substrates or cosubstrates.

29. A gene therapy composition, which comprises in a vehicle acceptable for gene therapy a nucleic acid construct which
    a) comprises an antisense nucleic acid against a coding nucleic acid as claimed in claim 6; or
    b) a ribozyme against a nucleic acid as claimed in claim 6; or
    c) codes for a specific PARP inhibitor.

30. A pharmaceutical composition comprising, in a pharmaceutically acceptable vehicle, at least one PARP protein as claimed in claim 1, at least one PARP binding partner or at least one coding nucleotide sequence

31. The use of low molecular weight PARP binding partners as claimed in claim 5 for the diagnosis or therapy of pathological states in the development and/or progress of which at least one PARP protein, or a polypeptide derived therefrom, is involved.

32. The use of low molecular weight PARP binding partners as claimed in claim 5 for the diagnosis or therapy of pathological states mediated by an energy deficit.

Novel poly(ADP-ribose) polymerase genes

The present invention relates to novel poly(ADP-ribose) polymerase (PARP) genes and to the proteins derived therefrom; antibodies with specificity for the novel proteins; pharmaceutical and gene therapy compositions which comprise products according to the invention; methods for the analytical determination of the proteins and nucleic acids according to the invention; methods for identifying effectors or binding partners of the proteins according to the invention; methods for determining the activity of such effectors and use thereof for the diagnosis or therapy of pathological states.

In 1966, Chambon and co-workers discovered a 116 kD enzyme which was characterized in detail in subsequent years and is now called PARP (EC 2.4.2.30) (poly(adenosine-5'-diphosphoribose) polymerase), PARS (poly(adenosine-5'-diphosphoribose) synthase) or ADPRT (adenosine-5'-diphosphoribose transferase). In the plant kingdom (*Arabidopsis thaliana*) a 72kD (637 amino acids) PARP was found in 1995 (Lepiniec L. et al., FEBS Lett 1995; 364(2): 103-8). It was not clear whether this shorter form of PARP is a plant-specific individuality or an artefact ("splice" variant or the like). The 116 kD PARP enzyme has to date been unique in animals and in man in its activity, which is described below. It is referred to as PARP1 below to avoid ambiguity.

The primary physiological function of PARP 1 appears to be its involvement in a complex repair mechanism which cells have developed to repair DNA strand breaks. The primary cellular response to a DNA strand break appears moreover to consist of PARP1-catalyzed synthesis of poly(ADP-ribose) from NAD^+ (cf. De Murcia, G. et al. (1994) TIBS, 19, 172).

PARP 1 has a modular molecular structure. Three main functional elements have been identified to date: an N-terminal 46 kD DNA binding domain; a central 22 kD automodification domain to which poly(ADP-ribose) becomes attached, with the PARP 1 enzyme activity decreasing with increasing elongation; and a C-terminal 54 kD NAD^+ binding domain. A leucine zipper region has been found within the automodification domain, indicating possible protein-protein interactions, only in the PARP from Drosophila. All PARPs known to date are presumably active as homodimers.

The high degree of organization of the molecule is reflected in the strong conservation of the amino acid sequence. Thus, 62% conservation of the amino acid sequence has been found for PARP 1

from humans, mice, cattle and chickens. There are greater structural differences from the PARP from Drosophila. The individual domains themselves in turn have clusters of increased conservation. Thus, the DNA binding region contains two so-called zinc fingers as subdomains (comprising motifs of the type $CX_2CX_{28/30}HX_2C$), which are involved in the Zn^{2+}-dependent recognition of DNA single strand breaks or single-stranded DNA overhangs (e.g. at the chromosome ends, the telomeres). The C-terminal catalytic domain comprises a block of about 50 amino acids (residues 859-908), which is about 100% conserved among vertebrates (PARP "signature"). This block binds the natural substrate NAD^+ and thus governs the synthesis of poly(ADP-ribose) (cf. de Murcia, loc.cit.). The GX_3GKG motif in particular is characteristic of PARPs in this block.

The beneficial function described above contrasts with a pathological one in numerous diseases (stroke, myocardial infarct, sepsis etc.). PARP is involved in cell death resulting from ischemia of the brain (Choi, D.W., (1997) Nature Medicine, 3, 10, 1073), of the myocardium (Zingarelli, B., et al (1997), Cardiovascular Research, 36, 205) and of the eye (Lam, T.T. (1997), Res. Comm. in Molecular Pathology and Pharmacology, 95, 3, 241). PARP activation induced by inflammatory mediators has also been observed in septic shock (Szabo, C., et al. (1997), Journal of Clinical Investigation, 100, 3, 723). In these cases, activation of PARP is accompanied by extensive consumption of NAD^+. Since four moles of ATP are consumed for the biosynthesis of one mole of NAD^+, the cellular energy supply decreases drasticallly. The consequence is cell death.

PARP1 inhibitors described in the abovementioned specialist literature are nicotinamide and 3-aminobenzamide. 3,4-Dihydro-5-[4-(1-piperidinyl)butoxy]-1(2H)-isoquinolone is disclosed by Takahashi, K., et al (1997), Journal of Cerebral Blood Flow and Metabolism 17, 1137. Further inhibitors are described, for example, in Banasik, M., et al. (1992) J. Biol. Chem., 267, 3, 1569 and Griffin, R.J., et al. (1995), Anti-Cancer Drug Design, 10, 507.

High molecular weight binding partners described for human PARP1 include the base excision repair (BER) protein XRCC1 (X-ray repair cross-complementing 1) which binds via a zinc finger motif and a BRCT (BRCA1 C-terminus) module (amino acids 372-524) (Masson, M., et al., (1998) Molecular and Cellular Biology, 18,6, 3563).

It is an object of the present invention, because of the diverse physiological and pathological functions of PARP, to provide novel PARP homologs. The reason for this is that the provision of homologous PARPs would be particularly important for developing novel targets for drugs, and novel drugs, in order to improve diagnosis and/or therapy of pathological states in which PARP, PARP homologs or substances derived therefrom are involved.

We have found that this object is achieved by providing PARP homologs, preferably derived from human and non-human mammals, having an amino acid sequence which has

a) a functional NAD^+ binding domain, i.e. a PARP "signature" sequence having the characteristic GX_3GKG motif; and

b) especially in the N-terminal sequence region, i.e. in the region of the first 200, such as, for example, in the region of the first 100, N-terminal amino acids, no PARP zinc finger sequence motifs of the general formula

$$CX_2CX_mHX_2C$$

in which

m is an integral value from 28 or 30, and the X radicals are, independently of one another, any amino acid;

and the functional equivalents thereof.

Since the PARP molecules according to the invention represent in particular functional homologs, they naturally also have a poly(ADP-ribose)-synthesizing activity. The NAD binding domain essentially corresponds to this activity and is localized to the C terminus.

Thus an essential characteristic of the PARPs according to the invention is the presence of a functional NAD^+ binding domain (PARP signature) which is located in the C-terminal region of the amino acid sequence (i.e. approximately in the region of the last 400, such as, for example, the last 350 or 300, C-terminal amino acids), in combination with an N-terminal sequence having no zinc finger motifs. Since the zinc finger motifs in known PARPs presumably contribute to recognition of the DNA breakages, it is to be assumed that the proteins according to the invention do not interact with DNA or do so in another way. It has been demonstrated by appropriate biochemical tests that the PARP2 according to the invention can be activated by 'activated DNA' (i.e. DNA after limited DNaseI digestion). It can be concluded from this further that the PARP2 according to the invention has DNA binding properties. However, the mechanism of the DNA binding and enzyme activation differs between the PARPs according to the invention and PARP1. Its DNA binding and enzyme activation is, as

mentioned, mediated by a characteristic zinc finger motif. No such motifs are present in the PARPs according to the invention. Presumably these properties are mediated by positively charged amino acids in the N-terminal region of the PARPs according to the invention. Since the 'activated DNA' (i.e. for example DNA after limited treatment with DNaseI) has a large number of defects (single strand breaks, single strand gaps, single-stranded overhangs, double strand breaks etc.), it is possible that although PARP1 and the PARPs according to the invention are activated by the same 'activated DNA', it is by a different subpopulation of defects (e.g. single strand gaps instead of single strand breaks).

The functional NAD^+ binding domain (i.e. catalytic domain) binds the substrate for poly-(ADP-ribose) synthesis. Consistent with known PARPs, the sequence motif $GX^1X^2X^3GKG$, in which G is glycine, K is lysine, and X^1, X^2 and X^3 are, independently of one another, any amino acid, is present in particular. However, as shown, surprisingly, by comparison of the amino acid sequences of the NAD^+ binding domains of PARP molecules according to the invention with previously disclosed human PARP1, the sequences according to the invention differ markedly from the known sequence for the NAD^+ binding domain.

A group of PARP molecules which is preferred according to the invention preferably has the following general sequence motif in the catalytic domain in common:

$PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11), in particular
$(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:12), preferably
$LLWHG(S/T)X_7IL(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFAX_3SKSAXY$ (SEQ ID NO:13)

in which (S/T) describes the alternative occupation of this sequence position by S or T, (I/V) describes the alternative occupation of this sequence position by I or V, and n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid. The last motif is also referred to as the "PARP signature" motif.

The automodification domain is preferably likewise present in the PARPs according to the invention. It can be located, for example, in the region from about 100 to 200 amino acids in front of the N-terminal end of the NAD^+ binding domain.

PARP homologs according to the invention may additionally comprise, N-terminally of the NAD^+ binding domain (i.e. about 30 to about 80 amino acids closer to the N terminus), a leucine zipper-like sequence motif of the general formula

$$(L/V)X_6LX_6LX_6L \quad \text{(SEQ ID NO:14)}$$

in which
(L/V) represents the alternative occupation of this sequence position by L or V, and the X radicals are, independently of one another, any amino acid. The leucine zipper motifs observed according to the invention differ distinctly in position from those described for PARP from Drosophila. Leucine zippers may lead to homodimers (two PARP molecules) or heterodimers (one PARP molecule with a binding partner differing therefrom).

The PARP homologs according to the invention preferably additionally comprise, N-terminally of the abovementioned leucine zipper-like sequence motifs, i.e. about 10 to 250 amino acid residues closer to the N terminus, at least another one of the following part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_bWGRVG$, (motif 1; SEQ ID NO:15)
$AX_3FXKX_4KTXNXWX_5FX_3PXK$, (motif 2; SEQ ID NO:16)
$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$, (motif 3; SEQ ID NO:17)
$FYTXIPHXFGX_3PP$, (motif 4; SEQ ID NO:18)
and
$KX_3LX_2LXDIEXAX_2L$ (motif 5; SEQ ID NO:19),

in which (D/E) describes the alternative occupation of this sequence position by D or E, (I/L) describes the alternative occupation of this sequence position by I or L, b is the integral value 10 or 11, and the X radicals are, independently of one another, any amino acid. It is most preferred for these motifs 1 to 5 all to be present in the stated sequence, with motif 1 being closest to the N terminus.

The abovementioned PARP signature motif is followed in the proteins according to the invention by at least another one of the following motifs:

$GX_3LXEVALG$ (motif 6; SEQ ID NO:20)
$GX_2SX_4GX_3PX_aLXGX_2V$ (motif 7; SEQ ID NO:21) and
$E(Y/F)X_2YX_3QX_4YLL$ (motif 8; SEQ ID NO:22)

in which (Y/F) describes the alternative occupation of this sequence position by Y or F, a is equal to 7 to 9 and X is in each case any amino acid. It is most preferred for the three

C-terminal motifs all to be present and in the stated sequence, with motif 8 being closest to the C terminus.

A preferred PARP structure according to the invention may be described schematically as follows:

Motifs 1 to 5/PARP signature/motifs 6 to 8 or
motifs 1 to 5/leucine zipper/PARP signature/motifs 6 to 8

it being possible for further amino acid residues, such as, for example, up to 40, to be arranged between the individual motifs and for further amino acid residues, such as, for example, up to 80, to be arranged at the N terminus and/or at the C terminus.

PARP homologs which are particularly preferred according to the invention are the proteins human PARP2, human PARP3, mouse PARP3 and the functional equivalents thereof. The protein referred to as human PARP2 comprises 570 amino acids (cf. SEQ ID NO:2). The protein referred to as human PARP3 possibly exists in two forms. Type 1 comprises 533 amino acids (SEQ ID NO:4) and type 2 comprises 540 amino acids (SEQ ID NO:6). The forms may arise through different initiation of translation. The protein referred to as mouse PARP3 exists in two forms which differ from one another by a deletion of 5 amino acids (15 bp). Type 1 comprises 533 amino acids (SEQ ID NO: 8) and type 2 comprises 528 amino acids (SEQ ID NO:10). The PARP-homologs of the present invention differ in their sequences significantly over said PARP protein of Arabidopsis thaliana (see above). For example, PARP2 and PARP3 do not comprise the plant PARP specific peptide sequence AAVLDQWIPD, corresponding to amino acid residues 143 to 152 of the Arabidopsis protein.

The invention further relates to the binding partners for the PARP homologs according to the invention. These binding partners are preferably selected from

a) antibodies and fragments such as, for example, Fv, Fab, $F(ab')_2$, thereof
b) protein-like compounds which interact, for example via the above leucine zipper region or another sequence section, with PARP, and
c) low molecular weight effectors which modulate a biological PARP function such as, for example, the catalytic PARP activity, i.e. NAD^+-consuming ADP ribosylation, or the binding to an activator protein or to DNA.

The invention further relates to nucleic acids comprising

a) a nucleotide sequence coding for at least one PARP homolog according to the invention, or the complementary nucleotide sequence thereof;
b) a nucleotide sequence which hybridizes with a sequence as specified in a), preferably under stringent conditions; or
c) nucleotide sequences which are derived from the nucleotide sequences defined in a) and b) through the degeneracy of the genetic code.

Nucleic acids which are suitable according to the invention comprise in particular at least one of the partial sequences which code for the abovementioned amino acid sequence motifs.

Nucleic acids which are preferred according to the invention comprise nucleotide sequences as shown in SEQ ID NO: 1 and 3, and, in particular, partial sequences thereof which are characteristic of PARP homologs according to the invention, such as, for example, nucleotide sequences comprising

a) nucleotides +3 to +1715 shown in SEQ ID NO:1;
b) nucleotides +242 to +1843 shown in SEQ ID NO:3;
c) nucleotides +221 to +1843 shown in SEQ ID NO:5;
d) nucleotides +112 to +1710 shown in SEQ ID NO:7; or
e) nucleotides +1 to +1584 shown in SEQ ID NO:9

or partial sequences of a), b), c), d) and e) which code for the abovementioned characteristic amino acid sequence motifs of the PARP homologs according to the invention.

The invention further relates to expression cassettes which comprise at least one of the above-described nucleotide sequences according to the invention under the genetic control of regulatory nucleotide sequences. These can be used to prepare recombinant vectors according to the invention, such as, for example, viral vectors or plasmids, which comprise at least one expression cassette according to the invention.

Recombinant microorganisms according to the invention are transformed with at least one of the abovementioned vectors.

The invention also relates to transgenic mammals transfected with a vector according to the invention.

The invention further relates to an in vitro detection method, which can be carried out homogeneously or heterogeneously, for PARP inhibitors, which comprises

a) incubating an unsupported or supported poly-ADP-ribosylatable target with a reaction mixture comprising
   a1) a PARP homolog according to the invention;
   a2) a PARP activator; and
   a3) a PARP inhibitor or an analyte in which at least one PARP inhibitor is suspected;
b) carrying out the polyADP ribosylation reaction; and
c) determining the polyADP ribosylation of the target qualitatively or quantitatively.

The detection method is preferably carried out by preincubating the PARP homolog with the PARP activator and the PARP inhibitor or an analyte in which at least one PARP inhibitor is suspected, for example for about 1-30 minutes, before carrying out the poly-ADP ribosylation reaction.

After activation by DNA with single strand breaks (referred to as "activated DNA" according to the invention), PARP poly-ADP ribosylates a large number of nuclear proteins in the presence of NAD. These proteins include, on the one hand, PARP itself, but also histones etc.

The poly-ADP-ribosylatable target preferably used in the detection method is a histone protein in its native form or a poly-ADP-ribosylatable equivalent derived therefrom. A histone preparation supplied by Sigma (SIGMA, catalogue No. H-7755; histone type II-AS from calf thymus, Luck, J. M., et al., J. Biol. Chem., 233, 1407 (1958), Satake K., et al., J. Biol. Chem, 235, 2801 (1960)) was used by way of example. It is possible in principle to use all types of proteins or parts thereof amenable to poly-ADP-ribosylation by PARP. These are preferably nuclear proteins, e.g. histones, DNA polymerase, telomerase or PARP itself. Synthetic peptides derived from the corresponding proteins can also act as target.

In the ELISA according to the invention it is possible to use amounts of histones in the range from about 0.1 µg/well to about 100 µg/well, preferably about 1 µg/well to about 10 µg/well. The amounts of the PARP enzyme are in a range from about 0.2 pmol/well to about 2 nmol/well, preferably from about 2 pmol/well to about 200 pmol/well, the reaction mixture comprising in each case 100 µg/well. Reductions to smaller wells and correspondingly smaller reaction volumes are possible.

In the HTRF assay according to the invention, identical amounts of PARP are employed, and the amount of histone or modified histones is in the range from about 2 ng/well to about 25 µg/well,

preferably about 25 ng/well to about 2.5 µg/well, the reaction mixture comprising in each case 50 µl/well. Reductions to smaller wells and correspondingly smaller reaction volumes are possible.

The PARP activator used according to the invention is preferably activated DNA.

Various types of damaged DNA can function as activator. DNA damage can be produced by digestion with DNases or other DNA-modifying enzymes (e.g. restriction endonucleases), by irradiation or other physical methods or chemical treatment of the DNA. It is further possible to simulate the DNA damage situation in a targeted manner using synthetic oligonucleotides. In the assays indicated by way of example, activated DNA from calf thymus was employed (Sigma, product No. D4522; CAS: 91080-16-9, prepared by the method of Aposhian and Kornberg using calf thymus DNA (SIGMA D-1501) and deoxyribonuclease type I (D-4263). Aposhian H. V. and Kornberg A., J. Biol. Chem., 237, 519 (1962)). The activated DNA was used in a concentration range from 0.1 to 1000 µg/ml, preferably from 1 to 100 µg/ml, in the reaction step.

The polyADP ribosylation reaction is started in the method according to the invention by adding NAD^+. The NAD concentrations were in a range from about 0.1 µM to about 10 mM, preferably in a range from about 10 µM to about 1 mM.

In the variant of the above method which can be carried out heterogeneously, the polyADP ribosylation of the supported target is determined using anti-poly(ADP-ribose) antibodies. To do this, the reaction mixture is separated from the supported target, washed and incubated with the antibody. This antibody can itself be labeled. However, as an alternative for detecting bound anti-poly(ADP-ribose) antibody a labeled secondary antibody or a corresponding labeled antibody fragment may be applied. Suitable labels are, for example, radiolabeling, chromophore- or fluorophore-labeling, biotinylation, chemiluminescence labeling, labeling with paramagnetic material or, in particular, enzyme labels, e.g. with horseradish peroxidase. Appropriate detection techniques are generally known to the skilled worker.

In the variant of the above process which can be carried out homogeneously, the unsupported target is labeled with an acceptor fluorophore. The target preferably used in this case is biotinylated histone, the acceptor fluorophore being coupled via avidin or streptavidin to the biotin groups of the histone. Particularly suitable as acceptor fluorophore are phycobiliproteins (e.g. phycocyanins, phycoerythrins), e.g. R-phycocyanin (R-PC), allophyco-

cyanin (APC), R-phycoerythrin (R-PE), C-phycocyanin (C-PC), B-phycoerythrin (B-PE) or their combinations with one another or with fluorescent dyes such as Cy5, Cy7 or Texas Red (Tandem system) (Thammapalerd, N. et al., Southeast Asian Journal of Tropical Medicine & Public Health, 27(2): 297-303 (1996); Kronick, M. N. et al., Clinical Chemistry, 29(9), 1582-1586 (1986); Hicks, J. M., Human Pathology, 15(2), 112-116 (1984)). The dye XL665 used in the examples is a crosslinked allophycocyanin (Glazer, A. N., Rev. Microbiol., 36, 173-198 (1982); Kronick, M. N., J. Imm. Meth., 92, 1-13 (1986); MacColl, R. et al., Phycobiliproteins, CRC Press, Inc., Boca Raton, Florida (1987); MacColl, R. et al., Arch. Biochem. Biophys., 208(1), 42-48 (1981)).

It is additionally preferred in the homogeneous method to determine the polyADP ribosylation of the unsupported target using anti-poly(ADP-ribose) antibody which is labeled with a donor fluorophore which is able to transfer energy to the acceptor fluorophore when donor and acceptor are close in space owing to binding of the labeled antibody to the polyADP-ribosylated histone. A europium cryptate is preferably used as donor fluorophore for the anti-poly(ADP-ribose) antibody.

Besides the europium cryptate used, other compounds are also possible as potential donor molecules. This may entail, on the one hand, modification of the cryptate cage. Replacement of the europium by other rare earth metals such as terbium is also conceivable. It is crucial that the fluorescence has a long duration to guarantee the time delay (Lopez, E. et al., Clin. Chem. 39/2, 196-201 (1993); US Patent 5,534,622).

The detection methods described above are based on the principle that there is a correlation between the PARP activity and the amount of ADP-ribose polymers formed on the histones. The assay described herein makes it possible to quantify the ADP-ribose polymers using specific antibodies in the form of an ELISA and an HTRF (homogenous time-resolved fluorescence) assay. Specific embodiments of these two assays are described in detail in the following examples.

The developed HTRF (homogeneous time-resolved fluorescence) assay system measures the formation of poly(ADP-ribose) on histones using specific antibodies. In contrast to the ELISA, this assay is carried out in homogeneous phase without separation and washing steps. This makes a higher sample throughput and a smaller susceptibility to errors possible. HTRF is based on the fluorescence resonance energy transfer (FRET) between two fluorophores. In a FRET assay, an excited donor fluorophore can

transfer its energy to an acceptor fluorophore when the two are close to one another in space. In HTRF technology, the donor fluorophore is a europium cryptate [(Eu)K] and the acceptor is XL665, a stabilized allophycocyanin. The europium cryptate is based on studies by Jean Marie Lehn (Strasbourg) (Lopez, E. et al., Clin. Chem. 39/2, 196-201 (1993); US Patent 5,534,622).

In a homogeneous assay, all the components are also present during the measurement. Whereas this has advantages for carrying out the assay (rapidity, complexity), it is necessary to preclude interference by assay components (inherent fluorescence, quenching by dyes etc.). HTRF precludes such interference by time-delayed measurement at two wavelengths (665 nm, 620 nm). The HTRF has a very long decay time and time-delayed measurement is therefore possible. There is no longer any interference from short-lived background fluorescence (e.g. from assay components or inhibitors of the substance library). In addition, measurement is always carried out at two wavelengths in order to compensate for quench effects of colored substances. HTRF assays can be carried out, for example, in 96- or 384-well microtiter plate format and are evaluated using a discovery HTRF microplate analyzer (Canberra Packard).

Also provided according to the invention are the following in vitro screening methods for binding partners for PARP, in particular for a PARP homolog according to the invention.

A first variant is carried out by

a1) immobilizing at least one PARP homolog on a support;

b1) contacting the immobilized PARP homolog with an analyte in which at least one binding partner is suspected; and

c1) determining, where appropriate after an incubation period, analyte constituents bound to the immobilized PARP homolog.

A second variant entails

a2) immobilizing on a support an analyte which comprises at least one possible binding partner for the PARP homolog;

b2) contacting the immobilized analyte with at least one PARP homolog for which a binding partner is sought; and

c3) examining the immobilized analyte, where appropriate after an incubation period, for binding of the PARP homolog.

The invention also relates to a method for the qualitative or quantitative determination of a nucleic acid encoding a PARP homolog, which comprises

a) incubating a biological sample with a defined amount of an exogenous nucleic acid according to the invention (e.g. with a length of about 20 to 500 bases or longer), hybridizing, preferably under stringent conditions, determining the hybridizing nucleic acids and, where appropriate, comparing with a standard; or

b) incubating a biological sample with a defined amount of oligonucleotide primer pairs with specificity for a PARP homolog-encoding nucleic acid, amplifying the nucleic acid, determining the amplification product and, where appropriate, comparing with a standard.

The invention further relates to a method for the qualitative or quantitative determination of a PARP homolog according to the invention, which comprises

a) incubating a biological sample with at least one binding partner specific for a PARP homolog,
b) detecting the binding partner/PARP complex and, where appropriate,
c) comparing the result with a standard.

The binding partner in this case is preferably an anti-PARP antibody or a binding fragment thereof, which carries a detectable label where appropriate.

The determination methods according to the invention for PARP, in particular for PARP homologs and for the coding nucleic acid sequences thereof, are suitable and advantageous for diagnosing sepsis- or ischemia-related tissue damage, in particular strokes, myocardial infarcts, diabetes or septic shock.

The invention further comprises a method for determining the efficacy of PARP effectors, which comprises

a) incubating a PARP homolog according to the invention with an analyte which comprises an effector of a physiological or pathological PARP activity; removing the effector again where appropriate; and
b) determining the activity of the PARP homolog, where appropriate after adding substrates or cosubstrates.

The invention further relates to gene therapy compositions which comprise in a vehicle acceptable for gene therapy a nucleic acid construct which

a) comprises an antisense nucleic acid against a coding nucleic acid according to the invention; or

b) a ribozyme against a noncoding nucleic acid according to the invention; or

c) codes for a specific PARP inhibitor.

The invention further relates to pharmaceutical compositions comprising, in a pharmaceutically acceptable vehicle, at least one PARP protein according to the invention, at least one PARP binding partner according to the invention or at least one coding nucleotide sequence according to the invention.

Finally, the invention relates to the use of binding partners of a PARP homolog for the diagnosis or therapy of pathological states in the development and/or progress of which at least one PARP protein, in particular a PARP homolog according to the invention, or a polypeptide derived therefrom, is involved. The binding partner used can be, for example, a low molecular weight binding partner whose molecular weight can be, for example, less than about 2000 dalton or less than about 1000 dalton.

The invention additionally relates to the use of PARP binding partners for the diagnosis or therapy of pathological states mediated by an energy deficit. An energy deficit for the purpose of the present invention is, in particular, a cellular energy deficit which is to be observed in the unwell patient systemically or in individual body regions, organs or organ regions, or tissues or tissue regions. This is characterized by an NAD and/or ATP depletion going beyond (above or below) the physiological range of variation of the NAD and/or ATP level and mediated preferably by a protein with PARP activity, in particular a PARP homolog according to the invention, or a polypeptide derived therefrom.

"Energy deficit-mediated disorders" for the purpose of the invention additionally comprise those in which tissue damage is attributable to cell death resulting from necrosis or apoptosis. The methods according to the invention are suitable for treating and preventing tissue damage resulting from cell damage due to apoptosis or necrosis; damage to nerve tissue due to ischemias and/or reperfusion; neurological disorders; neurodegenerative disorders; vascular stroke; for treating and preventing cardiovascular disorders; for treating other disorders or conditions such as, for example, age-related macular degeneration, AIDS or other immunodeficiency disorders; arthritis; atherosclerosis; cachexia; cancer; degenerative disorders of the skeletal muscles; diabetes; cranial trauma; inflammatory disorders of the gastrointestinal tract such as, for example, Crohn's disease; muscular dystrophy; osteoarthritis; osteoporosis; chronic and/or acute pain; kidney failure; retinal ischemia; septic shock (such as, for example,

endotoxin shock); aging of the skin or aging in general; general manifestations of aging. The methods according to the invention can additionally be employed for extending the life and the proliferative capacity of body cells and for sensitizing tumor cells in connection with irradiation therapy.

The invention particularly relates to the use of a PARP binding partner as defined above for the diagnosis or therapy (acute or prophylactic) of pathological states mediated by energy deficits and selected from neurodegenerative disorders, or tissue damage caused by sepsis or ischemia, in particular of neurotoxic disturbances, strokes, myocardial infarcts, damage during or after infarct lysis (e.g. with TPA, Reteplase or mechanically with laser or Rotablator) and of microinfarcts during and after heart valve replacement, aneurysm resections and heart transplants, trauma to the head and spinal cord, infarcts of the kidney (acute kidney failure, acute renal insufficiency or damage during and after kidney transplant), damages of skeletal muscle, infarcts of the liver (liver failure, damage during or after a liver transplant), peripheral neuropathies, AIDS dementia, septic shock, diabetes, neurodegenerative disorders occuring after ischemia, trauma (craniocerebral trauma), massive bleeding, subarachnoid hemorrhages and stroke, as well as neurodegenerative disorders like Alzheimer's disease, multi-infarct dementia, Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis, epilepsy, especially of generalized epileptic seizures such as petit mal and tonoclonic seizures and partial epileptic seizures, such as temporal lobe, and complex partial seizures, kidney failure, also in the chemotherapy of tumors and prevention of metastasis and for the treatment of inflammations and rheumatic disorders, e.g. of rheumatoid arthritis; further for the treatment of revascularization of critically narrowed coronary arteries and critically narrowed peripheral arteries, e.g. leg arteries.

"Ischemia" comprises for the purposes of the invention a localized undersupply of oxygen to a tissue, caused by blockage of arterial blood flow. Global ischemia occurs when the blood flow to the entire brain is interrupted for a limited period. This may be caused, for example, by cardiac arrest. Focal ischemia occurs when part of the brain is cut off from its normal blood supply. Focal ischemia may be caused by thromboembolic closure of a blood vessel, by cerebral trauma, edemas or brain tumor. Even transient ischemias can lead to wideranging neuronal damage. Although damage to "nerve tissue" may occur days or weeks after the start of the ischemia, some permanent damage (e.g. necrotic cell death) occurs in the first few minutes after interruption of the blood supply. This damage is caused, for example, by the neurotoxicity

of glutamate and follows secondary reperfusion, such as, for example, release of free radicals (e.g. oxygen free radicals, NO free radicals). Ischemias may likewise occur in other organs and tissues such as, for example, in the heart (myocardial infarct and other cardiovascular disorders caused by occlusion of the coronary arteries) or in the eye (ischemia of the retina).

The invention additionally relates to the use of an effective therapeutic amount of a PARP binding partner for influencing neuronal activity. "Neuronal activity" for the purposes of the invention may consist of stimulation of damaged neurons, promotion of neuronal regeneration or treatment of neuronal disorders.

"Neuronal damage" for the purposes of the invention comprises every type of damage to "nerve tissue" and every physical or mental impairment or death resulting from this damage. The cause of the damage may be, for example, metabolic, toxic, chemical or thermal in nature and includes by way of example ischemias, hypoxias, trauma, cerebrovascular damage, operations, pressure, hemorrhages, irradiation, vasospasms, neurodegenerative disorders, infections, epilepsy, perception disorders, disturbances of glutamate metabolism and the secondary effects caused thereby.

"Nerve tissue" for the purposes of the invention comprises the various components forming the nervous system, consisting of, inter alia, neurons, glia cells, astrocytes, Schwann cells, the vascular system inside and for supplying, the CNS, brain, brain stem, spinal cord, peripheral nervous system etc.

"Neuroprotective" for the purposes of the invention comprises the reduction, the cessation, the slowing down or the improvement of neuronal damage and the protection, the restoration and the regeneration of nerve tissue which was exposed to neuronal damage.

"Prevention of neurodegenerative disorders" includes the possibility of preventing, slowing down and improving neurodegenerative disorders in people for whom such a disorder has been diagnosed or who are included in appropriate risk groups for these neurodegenerative disorders. Treatments for people already suffering from symptoms of these disorders are likewise meant.

"Treatment" for the purposes of the invention comprises

(i) preventing a disorder, a disturbance or a condition in people with a predisposition thereto;

(ii) preventing a disorder, a disturbance or a condition by slowing down its advance; and

(iii) improving a disorder, a disturbance or a condition.

Examples of "neurological disorders" which can be treated by the methods according to the invention are neuralgias (trigeminal, glossopharyngeal), myasthenia gravis, muscular dystrophies, amyotrophic lateral sclerosis (ALS), progressive muscular atrophy, peripheral neuropathies caused by poisoning (e.g. lead poisoning), Guillain-Barré syndrome, Huntington's disease, Alzheimer's disease, Parkinson's disease, or plexus disorders. The methods according to the invention are preferably suitable for treating neurological disorders selected from peripheral neuropathies caused by physical injury or illness; cranial trauma such as, for example, traumatic brain injury; physical damage to the spinal cord; stroke associated with brain damage, such as vascular stroke in conjunction with hypoxia and brain damage, and cerebral reperfusion damage; demyelinating disorders (myelopathies, Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis).

The methods according to the invention can additionally be used for treating cardiovascular disorders. "Cardiovascular disorders" for the purposes of the invention comprise those which cause ischemias or are caused by ischemias or ischemia/reperfusion of the heart. Examples are coronary vessel disorders (for example atherosclerosis), angina pectoris, myocardial infarct, cardiovascular damage due to cardiac arrest or bypass operation.

The methods according to the invention can be used for treating cancer or for sensitizing cancer cells for irradiation therapy. The term "cancer" is to be understood in the widest sense. Modulators of the proteins according to the invention can be used as "anti-cancer therapy agents". For example, the methods can be used for treating types of cancer or tumor cells, such as ACTH-producing tumors, acute lymphatic or lymphoblastic leukemia; acute or chronic lymphocytic leukemia; acute nonlymphocytic leukemia; bladder cancer; brain tumors; breast cancer; cervical carcinoma; chronic myelocytic leukemia; bowel cancer; T-zone lymphoma; endometriosis; esophageal cancer; gall bladder cancer; Ewing's sarcoma; head and neck cancer; cancer of the tongue; Hodgkin's lymphoma; Kaposi's sarcoma; renal cancer; liver cancer; lung cancer; mesothelioma; multiple myeloma; neuroblastoma; non-Hodgkin lymphoma; osteosarcoma; ovarian carcinoma; glioblastoma; mammary carcinoma; cervical carcinoma; prostate cancer; pancreatic cancer; penis cancer; retinoblastoma; skin cancer; stomach

cancer; thyroid cancer; uterine carcinoma; vaginal carcinoma; Wilm's tumor; or trophoblastoma.

"Radiosensitizer" or "irradiation sensitizer" for the purposes of the invention relates to molecules which increase the sensitivity of the cells in the body to irradiation with electromagnetic radiation (for example X-rays) or speed up this irradiation treatment. Irradiation sensitizers increase the sensitivity of cancer cells to the toxic effects of the electromagnetic radiation. Those disclosed in the literature include mitomycin C, 5-bromodeoxyuridine and metronidazole. It is possible to use radiation with wavelengths in the range from 10^{-20} to 10 meters, preferably gamma rays (10^{-20} to 10^{-13} m), X-rays (10^{-11} to 10^{-9} m), ultraviolet radiation (10 nm to 400 nm), visible light (400 nm to 700 nm), infrared radiation (700 nm to 1 mm) and microwave radiation (1 mm to 30 cm).

Disorders which can be treated by such a therapy are, in particular, neoplastic disorders, benign or malignant tumors and cancer. The treatment of other disorders using electromagnetic radiation is likewise possible.

The present invention will now be described in more detail with reference to the appended figures. These show:

In Figure 1 a sequence alignment of human PARP (human PARP1) and two PARPs preferred according to the invention (human PARP2, human PARP3, murine PARP3). Sequence agreements between human PARP1 and human PARP2, human PARP3 or murine PARP3 are depicted within frames. The majority sequence is indicated over the alignment. The zinc finger motifs of human PARP1 are located in the sequence sections corresponding to amino acid residues 21 to 56 and 125 to 162;

In Figure 2 Northern blots with various human tissues to illustrate the tissue distribution of PARP2 and PARP3 molecules according to the invention. Lane 1: brain; lane 2: heart; lane 3: skeletal muscle; lane 4: colon; lane 5: thymus; lane 6: spleen; lane 7: kidney; lane 8: liver; lane 9: intestine; lane 10: placenta; lane 11: lung; lane 12: peripheral blood leukocytes; the respective position of the size standard (kb) is indicated.

In Figure 3 a Northern blot with further various human tissues to illustrate the tissue distribution of the PARP3 molecule according to the invention. Lane 1: heart; lane 2: brain; lane 3: placenta; lane 4: lung; lane 5: liver; lane 6: skeletal muscle; lane

7: kidney; lane 8: pancreas; the respective position of the size standard (kb) is indicated.

In Figure 4 a Western blot with various human tissues to illustrate the tissue distribution of the PARP3 molecule according to the invention at the protein level. Lane 1: heart; lane 2: lung; lane 3: liver; lane 4: spleen; lane 5: kidney; lane 6: colon; lane 7: muscle; lane 8: brain; the respective position of the size standard (kD) is indicated.

In Figure 5 a Western blot with various human tissues to illustrate the tissue distribution of the PARP3 molecule according to the invention. Lane 1: frontal cortex; lane 2: posterior cortex; lane 3: cerebellum; lane 4: hippocampus; lane 5: olfactory bulb; lane 6: striatum; lane 7: thalamus; lane 8: midbrain; lane 9: entorhinal cortex; lane 10: pons; lane 11: medulla; lane 12: spinal cord.

In Figure 6 a diagrammatic representation of the PARP assay (ELISA)

In Figure 7 a diagrammatic representation of the PARP assay (HTRF)

Further preferred embodiments of the invention are described in the following sections.

PARP homologs and functional equivalents

Unless stated otherwise, for the purposes of the present description amino acid sequences are indicated starting with the N terminus. If the one-letter code is used for amino acids, then G is glycine, A is alanine, V is valine, L is leucine, I is isoleucine, S is serine, T is threonine, D is aspartic acid, N is asparagine, E is glutamic acid, Q is glutamine, W is tryptophan, H is histidine, R is arginine, P is proline, K is lysine, Y is tyrosine, F is phenylalanine, C is cysteine and M is methionine.

The present invention is not confined to the PARP homologs specifically described above. On the contrary, those homologs which are functional equivalents thereof are also embraced. Functional equivalents comprise both natural, such as, for example, species-specific or organ-specific, and artificially produced variants of the proteins specifically described herein. Functional equivalents according to the invention differ by addition, substitution, inversion, insertion and/or deletion of one or more amino acid residues of human PARP2 (SEQ ID NO:2),

human PARP3 (SEQ ID NO: 4 and 6) and mouse PARP3 (SEQ ID:8 and 10), there being at least retention of the NAD-binding function of the protein mediated by a functional catalytic C-terminal domain. Likewise, the poly(ADP-ribose)-producing catalytic activity should preferably be retained. Functional equivalents also comprise where appropriate those variants in which the region similar to the leucine zipper is essentially retained.

It is moreover possible, for example, starting from the sequence for human PARP2 or human PARP3 to replace certain amino acids by those with similar physicochemical properties (bulk, basicity, hydrophobicity, etc.). It is possible, for example, for arginine residues to be replaced by lysine residues, valine residues by isoleucine residues or aspartic acid residues by glutamic acid residues. However, it is also possible for one or more amino acids to be exchanged in sequence, added or deleted, or several of these measures can be combined together. The proteins which have been modified in this way from the human PARP2 or human PARP3 sequence have at least 60%, preferably at least 75%, very particularly preferably at least 85%, homology with the starting sequence, calculated using the algorithm of Pearson and Lipman, Proc. Natl. Acad. Sci (USA) 85(8), 1988, 2444-2448.

The following homologies have been determined at the amino acid level and DNA level between human PARP1, 2 and 3 (FastA program, Pearson and Lipman, loc. cit.):

Amino acid homologies:

	Percent identity	Percent identity in PARP signature
PARP1/PARP2	41.97% (517)	86% (50)
PARP1/PARP3	33.81% (565)	53.1% (49)
PARP2/PARP3	35.20% (537)	53.1% (49)

Numbers in parentheses indicate the number of overlapping amino acids.

DNA Homologies:

	Percent identity in the ORF	Percent identity in PARP signature
PARP1/PARP2	60.81% (467)	77.85% (149)
PARP1/PARP3	58.81% (420)	59.02% (61)
PARP2/PARP3	60.22% (269)	86.36% (22)

Numbers in parentheses indicate the number of overlapping nucleotides.

The polypeptides according to the invention can be classified as homologous poly(ADP-ribose) polymerases on the basis of the great similarity in the region of the catalytic domain.

It is also essential to the invention that the novel PARP homologs do not have conventional zinc finger motifs. This means that these enzymes are not necessarily involved in DNA repair or are so in a way which differs from PARP1, but are still able to carry out their pathological mechanism (NAD^+ consumption and thus energy consumption due to ATP consumption). The strong protein expression, particularly of PARP3, observable in the Western blot suggests a significant role in the NAD consumption. This is particularly important for drug development. Potential novel inhibitors of the polymerases according to the invention can thus inhibit the pathological functions without having adverse effects on the desired physiological properties. This was impossible with inhibitors against the PARPs known to date since there was always also inhibition of the DNA repair function. The potentially mutagenic effect of known PARP inhibitors is thus easy to understand. It is also conceivable to design PARP inhibitors so that they efficiently inhibit all PARP homologs with high affinity. In this case, a potentiated effect is conceivable where appropriate.

The PARP homolog which is preferred according to the invention and is shown in SEQ ID NO:2 (human PARP2) can advantageously be isolated from human brain, heart, skeletal muscle, kidney and liver. The expression of human PARP2 in other tissues or organs is distinctly weaker.

The PARP homolog which is preferred according to the invention and is shown in SEQ ID NO: 4 and 6 (human PARP3) can advantageously be isolated from human brain (in this case very preferentially from the hippocampus), heart, skeletal muscle, liver or kidney. The expression of human PARP3 in other tissues or organs, such as muscle or liver, is distinctly weaker.

The skilled worker familiar with protein isolation will make use of the combination of preparative methodologies which is most suitable in each case for isolating natural PARPs according to the invention from tissues or recombinantly prepared PARPs according to the invention from cell cultures. Suitable standard preparative methods are described, for example, in Cooper, T.G., Biochemische Arbeitsmethoden, published by Walter de Gruyter, Berlin, New York or in Scopes, R. Protein Purification, Springer Verlag, New York, Heidelberg, Berlin.

The invention additionally relates to PARP2 and PARP3 homologs which, although they can be isolated from other eukaryotic species, i.e. invertebrates or vertebrates, especially other mammals such as, for example, mice, rats, cats, dogs, pigs, sheep, cattle, horses or monkeys, or from other organs such as, for example the myocardium, have the essential structural and functional properties predetermined by the PARPs according to the invention.

In particular, the human PARP2 which can be isolated from human brain, and its functional equivalents, are preferred agents for developing inhibitors of neurodegenerative diseases as for example stroke. This is because it can be assumed that drug development based on PARP2 as indicator makes it possible to develop inhibitors which are optimized for use in the human brain. However, it cannot be ruled out that inhibitors developed on the basis of PARP2 can also be employed for treating PARP-mediated pathological states in other organs, too (see tissue distribution of the proteins according to the invention).

PARP2 and presumably PARP3 are also, similar to PARP1, activated by damaged DNA, although by a presumably different mechanism. Significance in DNA repair is conceivable. Blockade of the PARPs according to the invention would also be beneficial in indications such as cancer (e.g. in the radiosensitization of tumor patients).

Another essential biological property of PARPs according to the invention and their functional equivalents is to be seen in their ability to bind an interacting partner. Human PARP2 and 3 differ

from previously disclosed PARPs from higher eukaryotes such as, in particular, mammals by having potential so-called leucine zipper motifs. This is a typical motif for protein-protein interactions. It is possible that these motifs permit modulation of PARP activity by an interacting partner. This additional structural element thus also provides a possible starting point for development of PARP effectors such as, for example, inhibitors.

The invention thus further relates to proteins which interact with PARP2 and/or 3, preferably those which bring about their activation or inactivation.

The invention further relates to proteins which still have the abovementioned ligand-binding activity and which can be prepared starting from the specifically disclosed amino acid sequences by targeted modifications.

It is possible, starting from the peptide sequence of the proteins according to the invention, to generate synthetic peptides which are employed, singly or in combination, as antigens for producing polyclonal or monoclonal antibodies. It is also possible to employ the PARP protein or fragments thereof for generating antibodies. The invention thus also relates to peptide fragments of PARP proteins according to the invention which comprise characteristic partial sequences, in particular those oligo- or polypeptides which comprise at least one of the abovementioned sequence motifs. Fragments of this type can be obtained, for example, by proteolytic digestion of PARP proteins or by chemical synthesis of peptides.

Novel specific PARP2 and PARP3 binding partners

Active and preferably selective inhibitors against the proteins according to the invention were developed using the specific assay systems described above for binding partners for PARP2 and PARP3. These inhibitors optionally are also active vis a vis PARP1.

Inhibitors provided according to the invention have a strong inhibitory activity on PARP2. The K_i values may in this case be less than about 1000 nM, such as less than about 700 nM, less than about 200 nM or less than about 30 nM, e.g. about 1 to 20 nM.

Inhibitors according to the invention may also have a surprising selectivity for PARP2. This is shown by the K_i(PARP1) : K_i(PARP2) ratio for such inhibitors according to the invention which is,

for example, greater than 3 or greater than 5, as for example greater than 10 or greater than 20.

An example which should be mentioned is 4-(N-(4-hydroxyphenyl)aminomethyl)-(2H)-dihydrophthalazine-1-one. The preparation of this and other analogous compounds may be performed according to Puodzhyunas et al., Pharm. Chem. J. 1973, 7, 566 or Mazkanowa et al., Zh. Obshch. Khim., 1958, 28, 2798, or Mohamed et al., Ind. J. Chem. B., 1994, 33, 769 each incorporated by reference.

The above identified compuound shows a Ki value of 113 nM for PARP2 and is eight times more selective for PARP2 than for PARP3.

Nucleic acids coding for PARP homologs:

Unless stated otherwise, nucleotide sequences are indicated in the present description from the 5′ to the 3′ direction.

The invention further relates to nucleic acid sequences which code for the abovementioned proteins, in particular for those having the amino acid sequence depicted in SEQ ID NO: 2, 4, 6, 8 and 10, but without being restricted thereto. Nucleic acid sequences which can be used according to the invention also comprise allelic variants which, as described above for the amino acid sequences, are obtainable by deletion, inversion, insertion, addition and/or substitution of nucleotides, preferably of nucleotides shown in SEQ ID NO: 1, 3, 7 and 9, but with essential retention of the biological properties and the biological activity of the corresponding gene product. Nucleotide sequences which can be used are obtained, for example, by nucleotide substitutions causing silent (without alteration of the amino acid sequence) or conservative amino acid changes (exchange of amino acids of the same size, charge, polarity or solubility).

Nucleic acid sequences according to the invention also embrace functional equivalents of the genes, such as eukaryotic homologs for example from invertebrates such as Caenorhabditis or Drosophila, or vertebrates, preferably from the mammals described above. Preferred genes are those from vertebrates which code for a gene product which has the properties essential to the invention as described above.

The nucleic acids according to the invention can be obtained in a conventional way by various routes:

For example, a genomic or a cDNA library can be screened for DNA which codes for a PARP molecule or a part thereof. For example, a cDNA library obtained from human brain, heart or kidney can be screened with a suitable probe such as, for example, a labeled single-stranded DNA fragment which corresponds to a partial sequence of suitable length selected from SEQ ID NO: 1 or 3, or sequence complementary thereto. For this purpose, it is possible, for example, for the DNA fragments of the library which have been transferred into a suitable cloning vector to be, after transformation into a bacterium, plated out on agar plates. The clones can then be transferred to nitrocellulose filters and, after denaturation of the DNA, hybridized with the labeled probe. Positive clones are then isolated and characterized.

The DNA coding for PARP homologs according to the invention or partial fragments can also be synthesized chemically starting from the sequence information contained in the present application. For example, it is possible for this purpose for oligonucleotides with a length of about 100 bases to be synthesized and sequentially ligated in a manner known per se by, for example, providing suitable terminal restriction cleavage sites.

The nucleotide sequences according to the invention can also be prepared with the aid of the polymerase chain reaction (PCR). For this, a target DNA such as, for example, DNA from a suitable full-length clone is hybridized with a pair of synthetic oligonucleotide primers which have a length of about 15 bases and which bind to opposite ends of the target DNA. The sequence section lying between them is then filled in with DNA polymerase. Repetition of this cycle many times allows the target DNA to be amplified (cf. White et al.(1989), Trends Genet. 5, 185).

The nucleic acid sequences according to the invention are also to be understood to include truncated sequences, single-stranded DNA or RNA of the coding and noncoding, complementary DNA sequence, mRNA sequences and cDNAs derived therefrom.

The invention further embraces nucleotide sequences hybridizing with the above sequences under stringent conditions. Stringent hybridization conditions for the purpose of the present invention exist when the hybridizing sequences have a homology of about 70 to 100%, such as, for example about 80 to 100% or 90 to 100% (preferably in an amino acid section of at least about 40, such as, for example, about 50, 100, 150, 200, 400 or 500 amino acids).

Stringent conditions for the screening of DNA, in particular cDNA banks, exist, for example, when the hybridization mixture is washed with 0.1X SSC buffer (20X SSC buffer = 3M NaCl, 0.3M sodium citrate, pH 7.0) and 0.1% SDS at a temperature of about 60°C.

Northern blot analyses are analyses are washed under stringent conditions with 0.1X SSC, 0,1% SDS at a temperature of about 65°C, for example.

Nucleic acid derivatives and expression constructs:

The nucleic acid sequences are also to be understood to include derivatives such as, for example, promoter variants or alternative splicing variants. The promoters operatively linked upstream of the nucleotide sequences according to the invention may moreover be modified by nucleotide addition(s) or substitution(s), inversion(s), insertion(s) and/or deletion(s), but without impairing the functionality or activity of the promoters. The promoters can also have their activity increased by modifying their sequence, or be completely replaced by more effective promoters even from heterologous organisms. The promoter variants described above are used to prepare expression cassettes according to the invention.

Specific examples of human PARP2 splicing variants which may be mentioned are:

Variant human PARP2a: Deletion of base pairs 766 to 904 (cf. SEQ ID NO:1). This leads to a frame shift with a new stop codon ("TAA" corresponding to nucleotides 922 to 924 in SEQ ID NO:1).
Variant human PARP2b: Insertion of
5'- gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg -3'
after nucleotide 204 (SEQ ID NO:1). This extends the amino acid sequence by the insertion: GMPGRSWASKRVS

Nucleic acid derivatives also mean variants whose nucleotide sequences in the region from -1 to -1000 in front of the start codon have been modified so that gene expression and/or protein expression is increased.

Besides the nucleotide sequence described above, the nucleic acid constructs which can be used according to the invention comprise in functional, operative linkage one or more other regulatory sequences, such as promoters, amplification signals, enhancers, polyadenylation sequences, origins of replication, reporter genes, selectable marker genes and the like. This linkage may,

depending on the desired use, lead to an increase or decrease in gene expression.

In addition to the novel regulatory sequences, it is possible for the natural regulatory sequence still to be present in front of the actual structural genes. This natural regulation can, where appropriate, be switched off by genetic modification, and the expression of the genes increased or decreased. However, the gene construct may also have a simpler structure, that is to say no additional regulatory signals are inserted in front of the structural genes, and the natural promoter with its regulation is not deleted. Instead, the natural regulatory sequence is mutated in such a way that regulation no longer takes place, and gene expression is enhanced or diminished. It is also possible to insert additional advantageous regulatory elements at the 3' end of the nucleic acid sequences. The nucleic acid sequences can be present in one or more copies in the gene construct.

Advantageous regulatory sequences for the expression method according to the invention are, for example, present in promoters such as cos, tac, trp, tet, trp-tet, lpp, lac, lpp-lac, lacIq, T7, T5, T3, gal, trc, ara, SP6, l-PR or the l-PL promoter, which are advantageously used in Gram-negative bacteria. Other advantageous regulatory sequences are present, for example, in the Gram-positive promoters amy and SPO2, in the yeast promoters ADC1, MFa, AC, P-60, CYC1, GAPDH or in the plant promoters CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or in the ubiquitin or phaseolin promoter.

It is possible in principle to use all natural promoters with their regulatory sequences. It is also possible and advantageous to use synthetic promoters.

Said regulatory sequences are intended to make specific expression of the nucleic acid sequences and protein expression possible. This may mean, for example, depending on the host organism that the gene is expressed or overexpressed only after induction, or that it is immediately expressed and/or overexpressed.

The regulatory sequences or factors may moreover preferably have a positive influence on, and thus increase or decrease, the expression. Thus, enhancement of the regulatory elements may advantageously take place at the level of transcription by using strong transcription signals such as promoters and/or enhancers.

However, it is also possible to enhance translation by, for example, improving the stability of the mRNA.

Enhancers mean, for example, DNA sequences which bring about increased expression via an improved interaction between RNA polymerase and DNA.

The recombinant nucleic acid construct or gene construct is, for expression in a suitable host organism, advantageously inserted into a host-specific vector which makes optimal expression of the genes in the host possible. Vectors are well known to the skilled worker and are to be found, for example, in "Cloning Vectors" (Pouwels P. H. et al., Ed., Elsevier, Amsterdam-New York-Oxford, 1985). Apart from plasmids, vectors also mean all other vectors known to the skilled worker, such as, for example, phages, viruses, such as SV40, CMV, baculovirus and adenovirus, transposons, IS elements, phasmids, cosmids, and linear or circular DNA. These vectors may undergo autonomous replication in the host organism or chromosomal replication.

Expression of the constructs:

The recombinant constructs according to the invention described above are advantageously introduced into a suitable host system and are expressed. Cloning and transfection methods familiar to the skilled worker are preferably used in order to bring about expression of said nucleic acids in the particular expression system. Suitable systems are described, for example, in Current Protocols in Molecular Biology, F. Ausubel et al., ed., Wiley Interscience, New York 1997.

Suitable host organisms are in principle all organisms which make it possible to express the nucleic acids according to the invention, their allelic variants, their functional equivalents or derivatives or the recombinant nucleic acid construct. Host organisms mean, for example, bacteria, fungi, yeasts, plant or animal cells. Preferred organisms are bacteria such as those of the genera Escherichia, such as, for example, Escherichia coli, Streptomyces, Bacillus or Pseudomonas, eukaryotic microorganisms such as Saccharomyces cerevisiae, Aspergillus, higher eukaryotic cells from animals or plants, for example Sf9 or CHO cells.

The gene product can also, if required, be expressed in transgenic organisms such as transgenic animals such as, in particular, mice, sheep, or transgenic plants. The transgenic organisms may also be so-called knock-out animals or plants in which the corresponding endogenous gene has been switched off,

such as, for example, by mutation or partial or complete deletion.

The combination of the host organisms and the vectors appropriate for the organisms, such as plasmids, viruses or phages, such as, for example, plasmids with the RNA polymerase/promoter system, phages λ, μ or other temperate phages or transposons and/or other advantageous regulatory sequences forms an expression system. The term expression systems preferably means, for example, a combination of mammalian cells such as CHO cells, and vectors, such as pcDNA3neo vector, which are suitable for mammalian cells.

As described above, the gene product can also be expressed advantageously in transgenic animals, e.g. mice, sheep, or transgenic plants. It is likewise possible to program cell-free translation systems with the RNA derived from the nucleic acid.

The gene product can also be expressed in the form of therapeutically or diagnostically suitable fragments. To isolate the recombinant protein it is possible and advantageous to use vector systems or oligonucleotides which extend the cDNA by certain nucleotide sequences and thus code for modified polypeptides which serve to simplify purification. Suitable modifications of this type are, for example, so-called tags which act as anchors, such as, for example, the modification known as the hexa-histidine anchor, or epitopes which can be recognized as antigens by antibodies (described, for example, in Harlow, E. and Lane, D., 1988, Antibodies: A Laboratory Manual. Cold Spring Harbor (N.Y.) Press). These anchors can be used to attach the proteins to a solid support such as, for example, a polymer matrix, which can, for example, be packed into a chromatography column, or to a microtiter plate or to another support.

These anchors can also at the same time be used to recognize the proteins. It is also possible to use for recognition of the proteins conventional markers such as fluorescent dyes, enzyme markers which form a detectable reaction product after reaction with a substrate, or radioactive markers, alone or in combination with the anchors for derivatizing the proteins.

Production of antibodies:

Anti-PARP2 antibodies are produced in a manner familiar to the skilled worker. Antibodies mean both polyclonal, monoclonal, human or humanized antibodies or fragments thereof, single chain antibodies or also synthetic antibodies, likewise antibody fragments such as Fv, Fab and $F(ab')_2$. Suitable production methods

are described, for example, in Campbell, A.M., Monoclonal Antibody Technology, (1987) Elsevier Verlag, Amsterdam, New York, Oxford and in Breitling, F. and Dübel, S., Rekombinante Antikörper (1997), Spektrum Akademischer Verlag, Heidelberg.

Further use of the coding sequence:

The present cDNA additionally provides the basis for cloning the genomic sequence of the novel PARP genes. This also includes the relevant regulatory or promoter sequence, which is available, for example, by sequencing the region located 5' upstream of the cDNA according to the invention or located in the introns of the genes. The cDNA sequence information is also the basis for producing antisense molecules or ribozymes with the aid of known methods (cf. Jones, J.T. and Sallenger, B.A. (1997) Nat. Biotechnol. 15, 902; Nellen, W. and Lichtenstein, C. (1993) TIBS, 18, 419). The genomic DNA can likewise be used to produce the gene constructs described above.

Another possibility of using the nucleotide sequence or parts thereof is to generate transgenic animals. Transgenic overexpression or genetic knock-out of the sequence information in suitable animal models may provide further valuable information about the (patho)physiology of the novel genes.

Therapeutic applications:

In situations where there is a prevailing deficiency of a protein according to the invention it is possible to employ several methods for replacement. On the one hand, the protein, natural or recombinant, can be administered directly or by gene therapy in the form of its coding nucleic acid (DNA or RNA). It is possible to use any suitable vectors for this, for example both viral and non-viral vehicles. Suitable methods are described, for example, by Strauss and Barranger in Concepts in Gene Therapy (1997), Walter de Gruyter, publisher. Another alternative is provided by stimulation of the endogenous gene by suitable agents.

It is also possible to block the turnover or the inactivation of PARPs according to the invention, for example by proteases. Finally, inhibitors or agonists of PARPs according to the invention can be employed.

In situations where a PARP is present in excess or is overactivated, various types of inhibitors can be employed. This inhibition can be achieved both by antisense molecules,

ribozymes, oligonucleotides or antibodies, and by low molecular weight compounds.

The active substances according to the invention, i.e. PARP proteins, nucleic acids and PARP binding partners such as, for example, antibodies or modulators, can be administered either as single therapeutic active substances or as mixtures with other therapeutic active substances. They can be administered as such, but in general they are administered in the form of pharmaceutical compositions, i.e. as mixtures of the active substance(s) with at least one suitable pharmaceutical carrier or diluent. The active substances or compositions can be administered in any way suitable for the particular therapeutic purpose, e.g. orally or parenterally.

The nature of the pharmaceutical composition and of the pharmaceutical carrier or diluent depends on the required mode of administration. Oral compositions can be, for example, in the form of tablets or capsules and may contain customary excipients such as binders (e.g. sirup, acacia, gelatin, sorbitol, tragacanth or polyvinylpyrrolidone), bulking agents (e.g. lactose, sugar, corn starch, calcium phosphate, sorbitol or glycine), lubricants (e.g. magnesium stearate, talc, polyethylene glycol or silica), disintegrants (e.g. starch) or wetting agents (e.g. sodium lauryl sulfate). Oral liquid products may be in the form of aqueous or oily suspensions, solutions, emulsions, sirups, elixirs or sprays etc. or may be in the form of dry powders for reconstitution with water or another suitable carrier. Liquid products of these types may contain conventional additives, for example suspending agents, flavorings, diluents or emulsifiers. It is possible to employ for parenteral administration solutions or suspensions with conventional pharmaceutical carriers. Parenteral administration of active substances according to the invention advantageously takes place using a liquid pharmaceutical composition which can be administered parenterally, in particular intravenously. This preferably contains an effective amount of at least one active substance, preferably in dissolved form, in a pharmaceutically acceptable carrier suitable for this purpose. Examples of pharmaceutical carriers suitable for this purpose are, in particular, aqueous solutions such as, for example, physiological saline, phosphate-buffered saline, Ringer's solution, Ringer's lactate solution and the like. The composition may moreover contain further additions such as antioxidants, chelating agents or antimicrobial agents.

The choice in each case of the dosage of the active substances according to the invention and the particular dosage schedule are subject to a decision of the treating physician. The latter will select a suitable dose and an appropriate dosage schedule depending on the chosen route of administration, on the efficacy of the medicine in each case, on the nature and severity of the disorder to be treated, and on the condition of the patient and his response to the therapy. Thus, for example, the pharmacologically active substances can be administered to a mammal (human or animal) in doses of about 0.5 mg to about 100 mg per kg of body weight and day. They can be administered in a single dose or in several doses.

Nontherapeutic applications:

The nucleic acids according to the invention, such as, for example, cDNA, the genomic DNA, the promoter, and the polypeptide, and partial fragments thereof, can also be used in recombinant or nonrecombinant form for developing various test systems.

For example, it is possible to establish a test system which is suitable for measuring the activity of the promoter or of the protein in the presence of a test substance. The methods of measurement in this case are preferably simple ones, e.g. colorimetric, luminometric, fluorimetric, immunological or radioactive, and allow preferably a large number of test substances to be measured rapidly. Tests of this type are suitable and advantageous for so-called high-throughput screening. These test systems allow test substances to be assessed for their binding to or their agonism, antagonism or inhibition of proteins according to the invention.

Determination of the amount, activity and distribution of the proteins according to the invention or their underlying mRNA in the human body can be used for the diagnosis, for the determination of the predisposition and for the monitoring of certain diseases. Likewise, the sequence of the cDNA and the genomic sequence may provide information about genetic causes of and predispositions to certain diseases. It is possible to use for this purpose both DNA/RNA probes and antibodies of a wide variety of types. The nucleotide sequences according to the invention or parts thereof can further be used in the form of suitable probes for detecting point mutations, deletions or insertions.

The proteins according to the invention can further be used to identify and isolate their natural ligands or interacting partners. The proteins according to the invention can additionally be used to identify and isolate artificial or synthetic ligands. For this purpose, the recombinantly prepared or purified natural protein can be derivatized in such a way that it has modifications which permit linkage to support materials. Proteins bound in this way can be incubated with various analytes, such as, for example, protein extracts or peptide libraries or other sources of ligands. Specifically bound peptides, proteins or low molecular weight, non-proteinogenous substances can be isolated and characterized in this way. Non-proteinogenous substances mean, for example, low molecular weight chemical substances which may originate, for example, from classical drug synthesis or from so-called substance libraries which have been synthesized combinatorially.

The protein extracts used are derived, for example, from homogenates of plants or parts of plants, microorganisms, human or animal tissues or organs.

Ligands or interacting partners can also be identified by methods like the yeast two-hybrid system (Fields, S. and Song, O. (1989) Nature, 340, 245). The expression banks which can be employed in this case may be derived, for example, from human tissues such as, for example, brain, heart, kidney etc.

The nucleic acid sequences according to the invention and the proteins encoded by them can be employed for developing reagents, agonists and antagonists or inhibitors for the diagnosis and therapy of chronic and acute diseases associated with the expression or activation of one of the protein sequences according to the invention, such as, for example, with increased or decreased expression thereof. The reagents, agonists, antagonists or inhibitors developed can subsequently be used to produce pharmaceutical preparations for the treatment or diagnosis of disorders. Examples of possible diseases in this connection are those of the brain, of the peripheral nervous system, of the cardiovascular system or of the eye, of septic shock, of rheumatoid arthritis, diabetes, acute kidney failure, or of cancer.

The relevance of the proteins according to the invention for said indications was verified using specific inhibitors in relevant animal models.

The invention is now illustrated in detail with reference to the following examples.

Example 1: Isolation of the PARP2 and PARP3 cDNA

The present cDNA sequences were found for the first time on sequence analysis of cDNA clones of a cDNA library from human brain (Human Brain 5'Stretch Plus cDNA Library, # HL3002a, Clontech). The mouse PARP3 clones were isolated from a "lambda triplex mouse brain cDNA library" (Clontech order No. ML5004t). The sequences of these clones are described in SEQ ID NO:1, 3, 7 and 9.

Example 2: Expression of PARP2 and PARP3 in human tissues

The expression of human PARP2 and human PARP3 was investigated in twelve different human tissues by Northern blot analysis. A Human Multiple Tissue Northern Blot (MTN™) supplied by Clontech (#7760-1 and #7780-1) was hybridized for this purpose with an RNA probe. The probe was produced by in vitro transcription of the corresponding cDNA of human PARP2 and human PARP3 in the presence of digoxigenin-labeled nucleotides in accordance with the manufacturer's method (BOEHRINGER MANNHEIM DIG Easy Hyb order No. 1603 558, DIG Easy Hyb method for RNA:RNA hybridization). The protocol was modified to carry out the prehybridization: 2x1h with addition of herring sperm DNA (10 mg/ml of hybridization solution). Hybridization then took place overnight with addition of herring sperm DNA (10 mg/ml of hybridization solution). The bands were detected using the CDP-Star protocol (BOEHRINGER MANNHEIM CDP-Star™ order No. 1685 627).

After stringent washing, the transcript of PARP2 was mainly detected in human brain, heart, skeletal muscle, kidney and liver. The transcript size of about 1.9 kb corresponds to the length of the cDNA determined (1.85kb) (cf. Figure 2(A)).

In other tissues or organs, human PARP2 expression is considerably weaker.

After stringent washing, the transcript of PARP3 was mainly detected in heart, brain, kidney, skeletal muscle and liver. Expression in other tissues (placenta, lung, pancreas) is distinctly weaker (cf. Figure 2(B)). There are at least 2 transcripts for human PARP3, which can presumably be explained by different polyadenylation sites or alternative splicing. Their size (about 2.2 kb and 2.5 kb respectively) corresponds to the length of the cDNA determined (2.3kb). Washing was carried out

with 0.2 x SSC/0.2% SDS at room temperature for 2 x 15 minutes and then with 0.1 x SSC/0.1% SDS at 65°C for 2 x 15 minutes (prepared from 20X SSC: 3M NaCl, 0.3M sodium citrate, pH 7.0).

Example 3: Production of antibodies

Specific antibodies against the proteins according to the invention were produced. These were used inter alia for analyzing the tissue distribution at the protein level of PARP2 and PARP3 by immunoblot (Western blot) analysis. Examples of the production of such antibodies are indicated below.

The following peptides were prepared by synthesis in the manner familiar to the skilled worker for the antibody production. In some cases, a cysteine residue was attached to the N or C terminals of the sequences in order to facilitate coupling to KLH (keyhole limpet hemocyanin).

PARP-2: NH_2-MAARRRRSTGGGRARALNES-CO_2H (amino acids 1-20; SEQ ID NO: 23)
NH_2-KTELQSPEHPLDQHYRNLHC-CO_2H (amino acids 335-353; SEQ ID NO: 24)

PARP-3: NH_2-CKGRQAGREEDPFRSTAEALK-CO_2H (amino acids 25-44 SEQ ID NO: 25)
NH_2-CKQQIARGFEALEALEEALK-CO_2H (amino acids 230-248; SEQ ID NO: 26)

The production of an anti-PARP3 antibody is described as a representative example.

For human PARP3, polyclonal antibodies were raised in rabbits using a synthetic peptide having the peptide sequence H_2N-KQQIARGFEALEALEEALK-CO_2H (SEQ ID NO: 27)(amino acids 230-248 of the human PARP3 protein sequence). The corresponding mouse sequence differs in this region only by one amino acid (H_2N-KQQIARGFEALEALEEAMK-CO_2H; SEQ ID NO: 28). A cysteine was also attached to the N terminus in order to make it possible for the protein to couple to KLH.

Rabbits were immunized a total of five times, at intervals of 7-14 days, with the KLH-peptide conjugate. The antiserum obtained was affinity-purified using the antigen. The specific IgG fraction was isolated from the serum using the respective peptides which, for this purpose, were initially immobilized on an affinity column in the manner familiar to the skilled worker. The respective antiserum was loaded onto this affinity column, and non-specifically sorbed proteins were eluted with buffer. The spe-

cifically bound IgG fraction was eluted with 0.2 M glycine/HCl buffer pH 2.2. The pH was immediately increased using a 1M TRIS/HCl buffer pH 7.5. The eluate containing the IgG fraction was mixed 1:1 (volume) with saturated ammonium sulfate solution and incubated at +4°C for 30 min to complete the precipitation. The resulting precipitate was centrifuged at 10,000 g and, after removal of the supernatant, dissolved in the minimum amount of PBS/TBS. The resulting solution was then dialyzed against PBS/TBS in the ratio 1:100 (volume). The antibodies were adjusted to a concentration of about 100 µg of IgG/ml. The PARP3 antibodies purified in this way had high specificity for PARP3. Whereas mouse PARP3 was recognized well, there was no observable cross-reaction with PARP1 or PARP2.

Example 4: Analysis of the tissue distribution by immunoblot (Western blot)

The tissue distribution at the protein level was also investigated for PARP2 and PARP3 by immunoblot (Western blot) analysis.

Preparation of the mouse tissues for protein gels:

Tissues or cells were homogenized using a Potter or Ultra-Turrax. For this, 0.5 g of tissue (or cells) was incubated in 5 ml of buffer (10 mM Tris-HCl pH 7.5, 1 mM EDTA, 6 mM $MgCl_2$), one tablet of protease inhibitor cocktail (Boehringer Mannheim, order No.: 1836153) and benzonase (purity grade I, MERCK) at 37°C for 30 min. Tissue samples from mice were produced for heart, lung, liver, spleen, kidney, intestine, muscle, brain and for human embryonic kidney cells (HEK293, human embryonal kidney).

Protein gels:

The NuPAGE system supplied by NOVEX was used according to the instructions for protein gels. Polyacrylamide gels (NuPAGE 4-12% BisTris, NOVEX NP 0321), running buffer (MES-Running Buffer, NOVEX NP 0002), antioxidant (NOVEX NP 0005), protein size standard (Multi Mark Multi Colored Standard, NOVEX LC 5725), sample buffer (NuPAGE LDS Sample Buffer (4X), NOVEX NP 0007) were used. The gels were run for 45 minutes at a voltage of 200 V.

Western blot:

Western blots were carried out using the NOVEX system in accordance with instructions. A nitrocellulose membrane (Nitrocellulose Pore size 45 µm, NOVEX LC 2001) was used. The transfer took 1 hour at a current of 200 mA. The transfer buffer consisted of 50 ml of

transfer buffer concentrate (NOVEX NP 0006), 1 ml of antioxidant (NOVEX NP 0002), 100 ml of analytical grade methanol and 849 ml of double-distilled water.

Besides the blots produced in this way, also used were premade blots, for example from Chemicon (mouse brain blot, Chemicon, catalog No.: NS 106 with the tissues 1. frontal cortex, 2. posterior cortex, 3. cerebellum, 4. hippocampus, 5. olfactory bulb, 6. striatum, 7. thalamus, 8. mid brain, 9. entorhinal cortex, 10. pons, 11. medulla, 12. spinal cord).

Antibody reaction with PARP3:

The Western blots were blocked in TBST (TBS + 0.3 % Tween 20) with 5% dry milk powder for at least 2 hours (TBS: 100 mM Tris pH 7.5, 200 mM NaCl). The antibody reaction with the primary antibody (dilution 1:1000) took place in TBST with 5% dry milk powder (see above) at room temperature for at least 2 hours or at 4°C overnight, with gentle agitation (vertical rotator). This was followed by washing three times in TBST for 5 minutes. Incubation with the secondary antibody (anti-rabbit IgG, peroxidase-coupled, SIGMA A-6154, dilution 1:2000) took place in TBST with 5% dry milk powder for 1 hour. This was followed by washing three times for 5 minutes each time as above. The subsequent detection was based on chemiluminescence using the SUPER BLAZE kit (Pierce, Signal BLAZE Chemiluminescent Substrate 34095) as stated by the manufacturer. The "Lumi-Film" (Chemiluminescent Detection Film, Boehringer order No: 1666916) was used. The films were developed for about 2 min (X-ray developer concentrate, ADEFO-Chemie GmbH), hydrated, fixed for about 4 min (Acidofix 85 g/l /AGFA), hydrated and then dried.

Example 5: Preparation of the enzymes

For comparison, human PARP1 was expressed recombinantly in the baculovirus system in the manner familiar to the skilled worker and partially purified as described (Shah et al., Analytical Biochemistry 1995, 227, 1-13). Bovine PARP1 in a purity of 30-50% (c= 0.22 mg/ml, spec. activity 170 nmol of ADP-ribose/min/mg of total protein at 25°C) was purchased from BIOMOL (order No. SE-165). Human and mouse PARP2 and PARP3 were expressed recombinantly in the baculovirus system (Bac-to-Bac system, BRL LifeScience). For this purpose, the appropriate cDNAs were cloned to the pFASTBAC-1 vector. Preparation of recombinant baculovirus DNA by recombination in E. coli was followed by transfection of insect cells (Sf9 or High-Five) with the appropriate recombinant baculovirus DNAs. Expression of the corresponding proteins was veri-

fied by Western blot analysis. Virus strains were amplified in the manner familiar to the skilled worker. Larger amounts of recombinant proteins were obtained by infecting 500 ml of insect cell culture (2 x 10^6 cells/ml) with viruses in an MOI (multiplicity of infection; ratio of viruses to cells) of 5-10 and incubating for 3 to 4 days. The insect cells were then pelleted by centrifugation, and the proteins were purified from the pellet.

The purification took place by classical methods of protein purification familiar to the skilled worker, detecting the enzymes with appropriate specific antibodies. In some cases, the proteins were also affinity-purified on a 3-aminobenzamide affinity column as described (Burtscher et al., Anal Biochem 1986, 152:285-290). The purity was >90%.

Example 6: Assay systems for determining the activity of PARP2 and PARP3 and the inhibitory action of effectors on PARP1, PARP2 and PARP3.

a) Production of antibodies against poly(ADP-ribose)

It is possible to use poly(ADP-ribose) as antigen for generating anti-poly(ADP-ribose) antibodies. The production of anti-poly(ADP-ribose) antibodies is described in the literature (Kanai Y et al. (1974) Biochem Biophys Res Comm 59:1, 300-306; Kawamaitsu H et al. (1984) Biochemistry 23, 3771-3777; Kanai Y et al. (1978) Immunology 34, 501-508).

The following were used, inter alia: anti-poly(ADP-ribose) antibodies (polyclonal antiserum, rabbits), BIOMOL; order No. SA-276, anti-poly(ADP-ribose) antibodies (monoclonal, mouse; clone 10H; hybridoma supernatant, affinity-purified).

The antisera or monoclonal antibodies obtained from hybridoma supernatant were purified by protein A affinity chromatography in the manner familiar to the skilled worker.

b) ELISA

Materials:

ELISA color reagent: TMB mix, SIGMA T-8540

A 96-well microtiter plate (FALCON Micro-Test III™ Flexible Assay Plate, # 3912) was coated with histones (SIGMA, H-7755). Histones were for this purpose dissolved in carbonate buffer (0.05M Na_2HCO_3; pH 9.4) in a concentration of 50 µg/ml. The individual

wells of the microtiter plate were each incubated with 150 µl of this histone solution at room temperature for at least 2 hours or at 4°C overnight. The wells are then blocked by adding 150 µl of a 1% BSA solution (SIGMA, A-7888) in carbonate buffer at room temperature for 2 hours. This is followed by three washing steps with washing buffer (0.05% Tween10 in 1x PBS; PBS (Phosphate buffered saline; Gibco, order No. 10010): 0.21g/l KH_2PO_4, 9g/l NaCl, 0.726g/l $Na_2HPO_4 \cdot 7H_2O$, pH 7.4). Washing steps were all carried out in a microtiter plate washer ("Columbus" microtiter plate washer, SLT-Labinstruments, Austria).

Required for the enzyme reaction were an enzyme reaction solution and a substrate solution, in each case as a premix. The absolute amount of these solutions depended on the intended number of assay wells.

Composition of the enzyme reaction solution per well:
- 4 µl of PARP reaction buffer (1M Tris-HCl pH 8.0, 100mM $MgCl_2$, 10mM DTT)
- 20ng of PARP1 (human or bovine) or 8ng PARP2 (human or mouse)
- 4 µl of activated DNA (1 mg/ml; SIGMA, D-4522)
- H_2O ad 40 µl

Composition of the substrate solution per well:
- 5 µl of PARP reaction buffer (10x)
- 0.8 µl of NAD solution (10mM, SIGMA N-1511)
- 44 µl H_2O

Inhibitors were dissolved in 1x PARP reaction buffer. DMSO, which was occasionally used to dissolve inhibitors in higher concentrations, was no problem up to a final concentration of 2%. For the enzyme reaction, 40 µl of the enzyme reaction solution were introduced into each well and incubated with 10 µl of inhibitor solution for 10 minutes. The enzyme reaction was then started by adding 50 µl of substrate solution per well. The reaction was carried out at room temperature for 30 minutes and then stopped by washing three times with washing buffer.

The primary antibodies employed were specific anti-poly(ADP-ribose) antibodies in a dilution of 1:5000. Dilution took place in antibody buffer (1% BSA in PBS; 0.05% Tween20). The incubation time for the primary antibodies was one hour at room temperature. After subsequently washing three times with washing buffer, incubation was carried out with the secondary antibody (anti-mouse IgG, Fab fragments, peroxidase-coupled, Boehringer Mannheim, order No. 1500.686; anti-rabbit IgG, peroxidase-coupled, SIGMA, order No. A-6154) in a dilution of 1:10,000 in antibody buffer at

room temperature for one hour. Washing three times with washing buffer was followed by the color reaction using 100 µl of color reagent (TMB mix, SIGMA) per well at room temperature for about 15 min. The color reaction was stopped by adding 100 µl of 2M H_2SO_4. This was followed by immediate measurement in an ELISA plate reader (EAR340AT "Easy Reader", SLT-Labinstruments, Austria) (450nm versus 620nm). The measurement principle is depicted diagrammatically in Figure 6.

Various concentrations were used to construct a dose-effect plot to determine the K_i value of an inhibitor. Values are obtained in triplicate for a particular inhibitor concentration. Arithmetic means are determined using Microsoft© Excel. The IC_{50} is determined using the Microcal© Origin Software (Vers. 5.0) ("Sigmoidal Fit"). Conversion of the IC_{50} value is calculated in this way into K_i values took place by using "calibration inhibitors". The "calibration inhibitors" were also measured in each analysis. The K_i values of the "calibration inhibitors" were determined in the same assay system by analysis of the Dixon diagram in the manner familiar to the skilled worker.

b) HTRF (homogenous time-resolved fluorescence) assay

In the HTRF PARP assay according to the invention, histones, as target proteins for modification by PARP, are labeled indirectly with an XL665 fluorophore. The anti poly(ADP ribose) antibody is directly labeled with a europium cryptate (anti-PAR-cryptate). If the XL665 fluorophore is in the direct vicinity in space, which is ensured by binding to the poly(ADP-ribose) on the histone, then energy transfer is possible. The emission at 665 nm is thus directly proportional to the amount of bound antibody, which in turn is equivalent to the amount of poly(ADP-ribose). The measured signal thus corresponds to the PARP activity. The measurement principle is depicted diagrammatically in Figure 7. The materials used are identical to those used in the ELISA (see above) unless expressly indicated.

Histones were dissolved in a concentration of 3 mg/ml in Hepes buffer (50mM, pH=7.5). Biotinylation took place with sulfo-NHS-LC-biotin (Pierce, #21335T). A molar ratio of 4 biotin molecules per histone was used. The incubation time was 90 minutes (RT). The biotinylated histones were then purified on a G25 SF HR10/10 column (Pharmacia, 17-0591-01) in Hepes buffer (50mM, pH=7.0) in order to remove excess biotinylation reagent. The anti-poly(ADP-ribose) antibody was labeled with europium cryptate using bifunctional coupling reagents (Lopez, E. et al., Clin. Chem. 39(2), 196-201 (1993); US Patent 5,534,622).

Purification took place on a G25SF HR10/30 column. A molar ratio of 3.1 cryptates per antibody was achieved. The yield was 25%. The conjugates were stored at -80°C in the presence of 0.1% BSA in phosphate buffer (0.1M, pH=7).

For the enzyme reaction, the following were pipetted into each well:
- 10 µl of PARP solution in PARP HTRF reaction buffer (50mM Tris-HCl pH 8.0, 10mM $MgCl_2$, 1mM DTT) with 20ng of PARP1 (human or bovine) or 8ng of PARP2 (human or mouse)
- 10 µl of activated DNA in PARP HTRF reaction buffer (50µg/ml)
- 10 µl of biotinylated histones in PARP HTRF reaction buffer (1.25µM)
- 10 µl of inhibitor in PARP HTRF reaction buffer

These reagents were incubated for 2 minutes before the reaction was started by adding
- 10 µl of NAD solution in PARP HTRF reaction buffer (41 µM/ml).

The reaction time was 30 minutes at room temperature.

The reaction was then stopped by adding
- 10 µl of PARP inhibitor (25 µM, K_i=10nM) in "Revelation" buffer (100mM Tris-HCl pH 7.2, 0.2M KF, 0.05% BSA).

The following were then added:
- 10 µl of EDTA solution (SIGMA, E-7889, 0.5M in H_2O)
- 100 µl of Sa-XL665 (Packard Instruments) in "Revelation" buffer (15-31.25nM)
- 50 µl of anti-PAR cryptate in "Revelation" buffer (1.6-3.3nM).

Measurement was then possible after 30 minutes (up to 4 hours). The measurement took place in a "discovery HTRF microplate analyzer" (Canberra Packard Instruments). The K_i values were calculated as described for the ELISA.

Example 7: Test systems for determining the therapeutic efficacy of PARP inhibitors

Novel PARP inhibitors can have their therapeutic efficacy checked in relevant pharmacological models. Examples of some suitable models are listed in Table 1.

Disorder	Model	Literature
Neurodegenerative disorders (stroke, Parkinson's, etc.)	NMDA excitotoxicity in mice or rats	See below for description
Stroke	Permanent MCAO ("middle cerebral arterial occlusion")	Tokime, T. et al., J. Cereb. Blood Flow Metab., 18(9): 991-7, 1998. Guegan, C., Brain Research. Molecular Brain Research, 55(1): 133-40, 1998.
	Transient, focal MCAO in rats or mice	Eliasson MJL et al., Nat Med 1997, 3:1089-1095. Endres, M et al., J Cereb Blood Flow Metab 1997, 17:1143-1151. Takahashi K et al., J Cereb Blood Flow Metab 1997, 17:1137-1142.
Parkinson's disease	MPTP (1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine) toxicity in mice/ rats	Cosi C, et al. , Brain Res. , 1998 809(1):58-67. Cosi C, et al. , Brain Res., 1996 729(2):264-9.
Myocardial infarct	Coronary vessel occlusion in rats, pigs or rabbits	Richard V, et al., Br. J. Pharmacol 1994, 113, 869-876. Thiemermann C, et al., Proc Natl Acad Sci U S A. 1997, 94(2):679-83. Zingarelli B, et al. , Cardiovasc Res. 1997, 36(2):205-15.
	Langendorf heart model in rats or rabbits	See below for description
Septic shock	Endotoxin shock in rats	Szabo C, et al., J Clin Invest, 1997, 100(3):723-35.

	Zymosan- or carrageenan-induced multiple organ failure in rats or mice	Szabo C, et al. J Exp Med. 1997, 186(7):1041-9.Cuzzocrea S, et al. Eur J Pharmacol. 1998, 342(1):67-76.
Rheumatoid arthritis	Adjuvant- or collagen-induced arthritis in rats or mice	Szabo C, et al., Proc Natl Acad Sci U S A. 1998, 95(7):3867-72.
Diabetes	Streptozotocin- and alloxan-induced or obesity-associated	Uchgata Y et al., Diabetes 1983, 32: 316-318.Masiello P et al., Diabetologia 1985, 28: 683-686.Shimabukuro M et al., J Clin Invest 1997, 100: 290-295.
Cancer	In vitro model; see below	Schlicker et al., 1999, 75(1), 91-100.

a) NMDA excitotoxicity model

Glutamate is the most important excitory neurotransmitter in the brain. Under normal conditions, glutamate is secreted into the synaptic cleft and stimulates the post-synaptic glutamate receptors, specifically the glutamate receptors of the "NMDA" and "AMPA" types. This stimulation plays a significant part in numerous functions of the brain, including learning, memory and motor control.

Under the conditions of acute and chronic neurodegeneration (e.g. stroke), however, there is a great increase in the presynaptic glutamate secretion, resulting in excessive stimulation of the receptors. This leads to death of the cells stimulated in this way. These increased glutamate activities occur in a number of neurological disorders or psychological disturbances and lead to states of overexcitation or toxic effects in the central nervous system (CNS) but also in the peripheral nervous system. Thus, glutamate is involved in a large number of neurodegenerative disorders, in particular neurotoxic disturbances following hypoxia, anoxia, ischemia and after lesions like those occurring after stroke and trauma, and stroke, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis (ALS; "Lou Gehring's disease"), cranial trauma, spinal cord trauma, peripheral neuropathies, AIDS dementia and Parkinson's disease. Another disease in which glutamate receptors are important is epilepsy (cf. Brain

Res Bull 1998; 46(4):281-309, Eur Neuropsychopharmacol 1998, 8(2):141-52.).

Glutamate effects are mediated through various receptors. One of these receptors is called the NMDA (N-methyl-D-aspartate) receptor after a specific agonist (Arzneim.Forschung 1990, 40, 511-514; TIPS, 1990, 11, 334-338; Drugs of the Future 1989, 14, 1059-1071). N-Methyl-D-aspartate is a strong agonist of a particular class of glutamate receptors ("NMDA" type). Stimulation of the NMDA receptor leads to influx of calcium into the cell and the generation of free radicals. The free radicals lead to DNA damage and activation of PARP. PARP in turn causes cell death through depletion of high-energy phosphates (NAD and ATP) in the cell. This explains the toxicity of NMDA. Treatment of animals with NMDA can therefore be regarded as a model of the abovementioned disorders in which excitotoxicity is involved.

Because of the importance of glutamate receptors in neurodegeneration, many pharmacological approaches to date have been directed at specific blocking of precisely these receptors. However, because of their importance in normal stimulus conduction, these approaches have proved to be problematic (side effects). In addition, stimulation of the receptors is an event which takes place very rapidly so that administration of the receptors often comes too late ("time window" problem). Thus there is a great need for novel principles of action and inhibitors of NMDA-related neurotoxicity.

Protection against cerebral overexcitation by excitatory amino acids (NMDA antagonism in mice) can be regarded as adequate proof of the activity of a pharmacological effector of PARP in disorders based on excitotoxicity. Intracerebral administration of excitatory amino acids (EAA) induces such massive overexcitation that it leads within a short time to convulsions and death of the animals (mice).

In the present case there was unilateral intracerebroventricular administration of 10 µl of a 0.035% strength aqueous NMDA solution 120 minutes after intraperitoneal (i.p.) administration of the test substance. These symptoms can be inhibited by systemic, e.g. intraperitoneal, administration of centrally acting drugs. Since excessive activation of EAA receptors in the central nervous system plays an important part in the pathogenesis of various neurological disorders, information can be gained from the detected EAA antagonism in vivo about possible therapeutic utilizability of the substances for such CNS disorders. An ED50 at which 50% of the animals are, due to preceding i.p.

administration of the measured substance, free of symptoms with a fixed dose of NMDA was determined as a measure of the activity of the substances.

b) Langendorf heart model (model for myocardial infarct)

Male Sprague-Dawley rats (bodyweight 300-400 g; origin Janvier, Le Genest-St-Isle, France) were used for the test. The rats were treated orally by gavage with the active substance or placebo (volume: 5 ml/kg). 50 minutes later, heparin is administered intraperitoneally (Liquemin N Roche, 125 IU/animal in 0.5 ml). The animals are anesthesized with Inactin® T133 (thiobetabarbital sodium 10%), fixed on the operating table, tracheotomized and ventilated with a "Harvard ventilatory pump" (40 beats/min, 4.5 ml/beat). Thoracotomy was followed by immediate catheterization of the aorta, removal of the heart and immediate retrograde perfusion. The hearts were perfused with a constant pressure of 75 mmHg, which is achieved using a "Gilson Miniplus 2 perfusion pump". Composition of the perfusate (mmol/l): NaCl 118, KCl 4.7, $CaCl_2$ x 2 H_2O 2.52, $MgSO_4$ x 7 H_2O 1.64, $NaHCO_3$ 24.88, KH_2PO_4 1.18, glucose 11. The temperature is kept at 37°C throughout the experiment. Functional parameters were continuously recorded using a "Gould 4-channel recorder". Measurements were made of the left-ventricular pressure (LVP; mmHg), LVEDP (mmHg), enzyme release (creatine kinase, mU/ml/g), coronary flow rate (ml/min), HR (pulse rate, min^{-1}). The left-ventricular pressure was measured using a liquid-filled latex balloon and a Statham23 Db pressure transducer. The volume of the balloon was initially adjusted to reach an LVEDP (left-ventricular end-diastolic pressure) of about 12 mmHg. The dP/dt_{max} (maximum pumping force) is derived from the pressure signal using a differentiator module. The heart rate was calculated from the pressure signal. The flow rate was determined using a drop counter (BMT Messtechnik GmbH Berlin). After an equilibration time of 20 minutes, the hearts were subjected to a 30-minute global ischemia by stopping the perfusate supply while keeping the temperature at 37°C. During the following 60-minute reperfusion period, samples of the perfusate were taken after 3, 5, 10, 15, 30, 45 and 60 min for analysis of creatine kinase (CK) activity. Means and standard deviations for the measured parameters were analyzed statistically (Dunnett test). The significance limit was $p=0.05$.

The experiment on rabbit hearts was carried out similarly. Male white New Zealand rabbits (obtained from: Interfauna) were used. The hearts were prepared as described above for the rat model. The perfusion pressure was set at a maximum of 60 mmHg and the flow rate at about 25ml/min. The equilibration time was about

30 min. The substance was administered by infusion directly upstream of the heart. 15 min after starting the infusion, a 30-minute global ischemia was caused by stopping the flow while maintaining the temperature of the heart. A 30-minute reperfusion followed. Perfusate was taken for investigation of CK activity before administration of the substance, after 15 min and at various times (5, 10, 15, 20, 30 min) during the reperfusion. The following parameters were measured: LVP (mmHg), LVEDP, LVdP/dt, PP (mmHg), HR (pulse rate; beats/min), CK activity (U/min/g heart weight).

c) Animal model for acute kidney failure

The protective effect of intravenous administration of PARP inhibitors (4 days) on the kidney function of rats with postischemic acute kidney failure was investigated.

Male Sprague-Dawley rats (about 330 g at the start of the experiments; breeder: Charles River) were used. 10-15 animals were employed per experimental group. Administration of active substance/placebo took place continuously with an osmotic micropump into the femoral vein. Orbital blood was taken (1.5 ml of whole blood) under inhalation anesthesia with enflurane (Ethrane Abbot, Wiesbaden).

After the initial measurements (blood sample) and determination of the amount of urine excreted in 24h, the rats were anesthetized ("Nembutal", pentobarbital sodium, Sanofi CEVA; 50mg/kg i.p., volume injected 1.0 ml/kg) and fastened on a heatable operating table (37°C). 125 IU/kg heparin (Liquemin N, Roche) were administered i.v. into the caudal vein. The abdominal cavity was opened and the right kidney was exposed. The branching-off renal artery was exposed and clamped off superiorly using bulldog clamps (Diefenbach 38mm). The left renal artery was likewise exposed and clamped off (superiorly, about half way to the kidney). During the operation, an osmotic micropump was implanted into the femoral vein. The intestine was reinserted and the fluid loss was compensated with luke-warm 0.9% NaCl. The animals were covered with a moist cloth and kept warm under red light. After 40 min, the appearance of the kidneys was recorded, and the clamps were removed, first the right then the left. The intestine was put back and 2 drops of antibiotic (Tardomyocel, Bayer) were added. The abdominal wall was closed with sterile cat gut (Ethicon No.4) and treated once more with 1 drop of antibiotic. The epidermis was sutured with sterile Ethibond Exel (Ethicon) No.3/0, and the

suture was sprayed with Nebacetin N (Yamanouchi) wound spray. A tenth of a daily dose of drug/placebo is given as i.v. bolus.

Samples and blood were taken for investigating biochemical parameters in the serum and urine: Na, K, creatinine, protein (only in urine), on days 1, 2 and 4 of the experiment. In addition, the feed and water consumption, bodyweight and urine volume were recorded. After 14 days, the animals were sacrificed and the kidneys were assessed.

The assessment excluded all animals which died of an infarct during the experiment or showed an infarct at necropsy on day 14. The creatinine clearance and the fractional sodium excretion were calculated as kidney function parameters, comparing treated animals with control and sham.

d) In vitro model for radiosensitization (tumor therapy)

MCF-7-cells (human breast carcinoma) were cultivated in Dulbecco's modified Eagle's medium with 10% heat-inactivated FCS and 2 mM L-glutamine. Cells were seeded out overnight in cell densities of 100, 1000 or 10,000 cells per well in a 6-well plate and then exposed to ionizing radiation with a dose in the range from 0 to 10 Gy (^{137}Cs, Shepard Mark, model I-68A, dose rate 3.28 Gy/min). 10 days after the irradiation, the experiment was assessed, counting colonies with fifty cells as positive.

e) Stroke model (focal cerebral ischemia; MCA (middle cerebral artery) occlusion on a rat)

A focal ischemia was performed by means of cauterisation of the right distal MCA on Sprague-Dawley or Long-Evans rats. The rats may be treated before or after the beginning of the MCA occlusion with modulators of the proteins of the invention. As a rule, doses of 1-10 mg/kg are chosen (bolus application), optionally followed by a continuous infusion of 0.5-5 mg/kg/h.

The rats are anesthetised with halothane in a mixture of 70 % nitrogen and 30 % oxygen (4% at initial phase and 0.8-1.2 % during the operation). The body temperature was permanently measured rectally and was kept constant at 37.5 °C ± 0.5 °C by means of a controllable heating blanket. Moreover, arterial blood pressure, arterial pH, ($Pa(O_2)$) and ($Pa(CO_2)$) were optionally measured by means of a tail vein catheder. Thereafter, the focal iscehmia was carried out using the method of Chen et al. (Stroke 17: 738-743; 1986) or Liu et al. (Am. J. Physiol. 256: H589-593; 1989) by means of continuous cauterisation of the distal part of the right

MCA. When the operation was terminated, the animals were kept in a warm environment for a further 24 hours. Then they were killed with the use of CO_2 and decapitated. Their brains were taken, shock-frozen (dry ice or liquid nitrogen) and stored at -80 °C. The brains were cut into 0.02 mm thick slices and every 20th cut was used for the subsequent analysis. The corresponding cuts are stained with cresyl violet (Nissl staining). Alternatively, TTC (2,3,4-triphenyltetrazoliumchloride) may be used for staining. The infarct volume may then be analysed under a microscope. For exact quantification, a computer-based image analyzing software may be used (J. Cereb. Clood Flow Metabol. 10: 290-293; 1990).

f) Septic shock

Groups of 10 male C57/BL mice (body weight 18-20 g) are treated with LPS (lipopolysaccharide, from E. coli, LD_{100} 20 mg/animal i. v.) plus galactosamine (20 mg/animal i. v.). the substance to be tested is applied i. p. or i. v. during three succeeding days (e. g. 1-10 mg/kg), with the first dose being administered 30 minutes after the LPS treatment. The death rate is determined every 12 hours. Alternatively, the substance may also be applied in several doses spread over the days.

g) Determination of altered gene expression in aging cells

The aging of cells is simulated by changing the cell culture media from the complete medium with a reduced serum concentration and thereafter is analysed by means of quantitative PCR or Northern Blotting (Linskens et al., Nucleic Acids Res. 1995, 23(16): 3244-51). As typical markers for the aging of the skin for example collagen or elastin may be used. Human fibroblasts or fibroblast cell lines are used which simulate the aging of the skin. Modulators of the proteins of the invention are added to the medium and their effect on the changing of the gene expression is observed. An increased production of elastin in cells with a reduced aging process caused by means of said modulators may be observed.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: BASF Aktiengesellschaft
(B) STREET:
(C) CITY: Ludwigshafen
(E) COUNTRY: Deutschland
(F) POSTAL CODE (ZIP): 67065

(ii) TITLE OF INVENTION: Neue Poly ADP Ribose Polymerase Gene

(iii) NUMBER OF SEQUENCES: 28

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC DOS/MS DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:
(F) TISSUE TYPE: Brain

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:3..1715
(D) OTHER INFORMATION:/product= "Poly ADP Ribose Polymerase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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   Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg
     1               5                  10                  15

GCA TTA AAT GAA AGC AAA AGA GTT AAT AAT GGC AAC ACG GCT CCA GAA          95
Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu
                 20                  25                  30
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GAC TCT TCC CCT GCC AAG AAA ACT CGT AGA TGC CAG AGA CAG GAG TCG        143
Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser
            35                  40                  45

AAA AAG ATG CCT GTG GCT GGA GGA AAA GCT AAT AAG GAC AGG ACA GAA        191
Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu
        50                  55                  60

GAC AAG CAA GAT GAA TCT GTG AAG GCC TTG CTG TTA AAG GGC AAA GCT        239
Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala
    65                  70                  75

CCT GTG GAC CCA GAG TGT ACA GCC AAG GTG GGG AAG GCT CAT GTG TAT        287
Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr
80                  85                  90                  95

TGT GAA GGA AAT GAT GTC TAT GAT GTC ATG CTA AAT CAG ACC AAT CTC        335
Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu
                100                 105                 110

CAG TTC AAC AAC AAC AAG TAC TAT CTG ATT CAG CTA TTA GAA GAT GAT        383
Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp
            115                 120                 125

GCC CAG AGG AAC TTC AGT GTT TGG ATG AGA TGG GGC CGA GTT GGG AAA        431
Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys
        130                 135                 140

ATG GGA CAG CAC AGC CTG GTG GCT TGT TCA GGC AAT CTC AAC AAG GCC        479
Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala
    145                 150                 155

AAG GAA ATC TTT CAG AAG AAA TTC CTT GAC AAA ACG AAA AAC AAT TGG        527
Lys Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp
160                 165                 170                 175

GAA GAT CGA GAA AAG TTT GAG AAG GTG CCT GGA AAA TAT GAT ATG CTA        575
Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu
                180                 185                 190

CAG ATG GAC TAT GCC ACC AAT ACT CAG GAT GAA GAG GAA ACA AAG AAA        623
Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys
            195                 200                 205

GAG GAA TCT CTT AAA TCT CCC TTG AAG CCA GAG TCA CAG CTA GAT CTT        671
Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu
        210                 215                 220

CGG GTA CAG GAG TTA ATA AAG TTG ATC TGT AAT GTT CAG GCC ATG GAA        719
Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu
    225                 230                 235

GAA ATG ATG ATG GAA ATG AAG TAT AAT ACC AAG AAA GCC CCA CTT GGG        767
Glu Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly
240                 245                 250                 255

AAG CTG ACA GTG GCA CAA ATC AAG GCA GGT TAC CAG TCT CTT AAG AAG        815
Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys
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                  260                 265                 270

ATT GAG GAT TGT ATT CGG GCT GGC CAG CAT GGA CGA GCT CTC ATG GAA       863
Ile Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu
            275                 280                 285

GCA TGC AAT GAA TTC TAC ACC AGG ATT CCG CAT GAC TTT GGA CTC CGT       911
Ala Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg
        290                 295                 300

ACT CCT CCA CTA ATC CGG ACA CAG AAG GAA CTG TCA GAA AAA ATA CAA       959
Thr Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln
    305                 310                 315

TTA CTA GAG GCT TTG GGA GAC ATT GAA ATT GCT ATT AAG CTG GTG AAA      1007
Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys
320                 325                 330                 335

ACA GAG CTA CAA AGC CCA GAA CAC CCA TTG GAC CAA CAC TAT AGA AAC      1055
Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn
                340                 345                 350

CTA CAT TGT GCC TTG CGC CCC CTT GAC CAT GAA AGT TAC GAG TTC AAA      1103
Leu His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys
            355                 360                 365

GTG ATT TCC CAG TAC CTA CAA TCT ACC CAT GCT CCC ACA CAC AGC GAC      1151
Val Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp
        370                 375                 380

TAT ACC ATG ACC TTG CTG GAT TTG TTT GAA GTG GAG AAG GAT GGT GAG      1199
Tyr Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu
    385                 390                 395

AAA GAA GCC TTC AGA GAG GAC CTT CAT AAC AGG ATG CTT CTA TGG CAT      1247
Lys Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His
400                 405                 410                 415

GGT TCC AGG ATG AGT AAC TGG GTG GGA ATC TTG AGC CAT GGG CTT CGA      1295
Gly Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg
                420                 425                 430

ATT GCC CCA CCT GAA GCT CCC ATC ACA GGT TAC ATG TTT GGG AAA GGA      1343
Ile Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly
            435                 440                 445

ATC TAC TTT GCT GAC ATG TCT TCC AAG AGT GCC AAT TAC TGC TTT GCC      1391
Ile Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala
        450                 455                 460

TCT CGC CTA AAG AAT ACA GGA CTG CTG CTC TTA TCA GAG GTA GCT CTA      1439
Ser Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu
    465                 470                 475

GGT CAG TGT AAT GAA CTA CTA GAG GCC AAT CCT AAG GCC GAA GGA TTG      1487
Gly Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu
480                 485                 490                 495

CTT CAA GGT AAA CAT AGC ACC AAG GGG CTG GGC AAG ATG GCT CCC AGT      1535
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```
Leu Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser
                500                 505                 510

TCT GCC CAC TTC GTC ACC CTG AAT GGG AGT ACA GTG CCA TTA GGA CCA      1583
Ser Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro
            515                 520                 525

GCA AGT GAC ACA GGA ATT CTG AAT CCA GAT GGT TAT ACC CTC AAC TAC      1631
Ala Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr
        530                 535                 540

AAT GAA TAT ATT GTA TAT AAC CCC AAC CAG GTC CGT ATG CGG TAC CTT      1679
Asn Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu
    545                 550                 555

TTA AAG GTT CAG TTT AAT TTC CTT CAG CTG TGG TGA ATGTTGATAT          1725
Leu Lys Val Gln Phe Asn Phe Leu Gln Leu Trp  *
560                 565                 570

TAAATAAACC AGAGATCTGA TCTTCAAGCA AGAAAATAAG CAGTGTTGTA CTTGTGAATT    1785

TTGTGATATT TTATGTAATA AAAACTGTAC AGGTCTAAAA AAAAAAAAAA AAAAAAAA      1843
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 571 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala
  1               5                  10                  15

Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu Asp
             20                  25                  30

Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser Lys
         35                  40                  45

Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu Asp
     50                  55                  60

Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala Pro
 65                  70                  75                  80

Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr Cys
                 85                  90                  95

Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu Gln
            100                 105                 110

Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp Ala
        115                 120                 125

Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met
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    130                 135                 140
Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala Lys
145                 150                 155                 160
Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp Glu
                165                 170                 175
Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu Gln
            180                 185                 190
Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys Glu
        195                 200                 205
Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu Arg
    210                 215                 220
Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu Glu
225                 230                 235                 240
Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly Lys
                245                 250                 255
Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile
            260                 265                 270
Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu Ala
        275                 280                 285
Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg Thr
    290                 295                 300
Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln Leu
305                 310                 315                 320
Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys Thr
                325                 330                 335
Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn Leu
            340                 345                 350
His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys Val
        355                 360                 365
Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp Tyr
    370                 375                 380
Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu Lys
385                 390                 395                 400
Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His Gly
                405                 410                 415
Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
            420                 425                 430
Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile
        435                 440                 445
Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser
```

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    450                 455                 460

Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly
465                 470                 475                 480

Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu
                485                 490                 495

Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser
            500                 505                 510

Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala
        515                 520                 525

Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn
    530                 535                 540

Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu
545                 550                 555                 560

Lys Val Gln Phe Asn Phe Leu Gln Leu Trp  *
                565                 570
```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:242..1843
(D) OTHER INFORMATION:/product= "Poly ADP Ribose Polymerase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
TGGGACTGGT CGCCTGACTC GGCCTGCCCC AGCCTCTGCT TCACCCCACT GGTGGCCAAA      60

TAGCCGATGT CTAATCCCCC ACACAAGCTC ATCCCCGGCC TCTGGGATTG TTGGGAATTC     120

TCTCCCTAAT TCACGCCTGA GGCTCATGGA GAGTTGCTAG ACCTGGGACT GCCCTGGGAG     180

GCGCACACAA CCAGGCCGGG TGGCAGCCAG GACCTCTCCC ATGTCCCTGC TTTTCTTGGC     240

C ATG GCT CCA AAG CCG AAG CCC TGG GTA CAG ACT GAG GGC CCT GAG          286
  Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu
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                575                 580                 585

AAG AAG AAG GGC CGG CAG GCA GGA AGG GAG GAG GAC CCC TTC CGC TCC      334
Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser
            590                 595                 600

ACC GCT GAG GCC CTC AAG GCC ATA CCC GCA GAG AAG CGC ATA ATC CGC      382
Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg
        605                 610                 615

GTG GAT CCA ACA TGT CCA CTC AGC AGC AAC CCC GGG ACC CAG GTG TAT      430
Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr
    620                 625                 630

GAG GAC TAC AAC TGC ACC CTG AAC CAG ACC AAC ATC GAG AAC AAC AAC      478
Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn
635                 640                 645                 650

AAC AAG TTC TAC ATC ATC CAG CTG CTC CAA GAC AGC AAC CGC TTC TTC      526
Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe
                655                 660                 665

ACC TGC TGG AAC CGC TGG GGC CGT GTG GGA GAG GTC GGC CAG TCA AAG      574
Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys
            670                 675                 680

ATC AAC CAC TTC ACA AGG CTA GAA GAT GCA AAG AAG GAC TTT GAG AAG      622
Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys
        685                 690                 695

AAA TTT CGG GAA AAG ACC AAG AAC AAC TGG GCA GAG CGG GAC CAC TTT      670
Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe
    700                 705                 710

GTG TCT CAC CCG GGC AAG TAC ACA CTT ATC GAA GTA CAG GCA GAG GAT      718
Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp
715                 720                 725                 730

GAG GCC CAG GAA GCT GTG GTG AAG GTG GAC AGA GGC CCA GTG AGG ACT      766
Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr
                735                 740                 745

GTG ACT AAG CGG GTG CAG CCC TGC TCC CTG GAC CCA GCC ACG CAG AAG      814
Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys
            750                 755                 760

CTC ATC ACT AAC ATC TTC AGC AAG GAG ATG TTC AAG AAC ACC ATG GCC      862
Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala
        765                 770                 775

CTC ATG GAC CTG GAT GTG AAG AAG ATG CCC CTG GGA AAG CTG AGC AAG      910
Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys
    780                 785                 790

CAA CAG ATT GCA CGG GGT TTC GAG GCC TTG GAG GCG CTG GAG GAG GCC      958
Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala
795                 800                 805                 810

CTG AAA GGC CCC ACG GAT GGT GGC CAA AGC CTG GAG GAG CTG TCC TCA     1006
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Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser
                815                 820                 825

CAC TTT TAC ACC GTC ATC CCG CAC AAC TTC GGC CAC AGC CAG CCC CCG      1054
His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro
            830                 835                 840

CCC ATC AAT TCC CCT GAG CTT CTG CAG GCC AAG AAG GAC ATG CTG CTG      1102
Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu
        845                 850                 855

GTG CTG GCG GAC ATC GAG CTG GCC CAG GCC CTG CAG GCA GTC TCT GAG      1150
Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu
    860                 865                 870

CAG GAG AAG ACG GTG GAG GAG GTG CCA CAC CCC CTG GAC CGA GAC TAC      1198
Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr
875                 880                 885                 890

CAG CTT CTC AAG TGC CAG CTG CAG CTG CTA GAC TCT GGA GCA CCT GAG      1246
Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu
                895                 900                 905

TAC AAG GTG ATA CAG ACC TAC TTA GAA CAG ACT GGC AGC AAC CAC AGG      1294
Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg
            910                 915                 920

TGC CCT ACA CTT CAA CAC ATC TGG AAA GTA AAC CAA GAA GGG GAG GAA      1342
Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu
        925                 930                 935

GAC AGA TTC CAG GCC CAC TCC AAA CTG GGT AAT CGG AAG CTG CTG TGG      1390
Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp
    940                 945                 950

CAT GGC ACC AAC ATG GCC GTG GTG GCC GCC ATC CTC ACT AGT GGG CTC      1438
His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu
955                 960                 965                 970

CGC ATC ATG CCA CAT TCT GGT GGG CGT GTT GGC AAG GGC ATC TAC TTT      1486
Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe
                975                 980                 985

GCC TCA GAG AAC AGC AAG TCA GCT GGA TAT GTT ATT GGC ATG AAG TGT      1534
Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys
            990                 995                1000

GGG GCC CAC CAT GTC GGC TAC ATG TTC CTG GGT GAG GTG GCC CTG GGC      1582
Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly
        1005                1010                1015

AGA GAG CAC CAT ATC AAC ACG GAC AAC CCC AGC TTG AAG AGC CCA CCT      1630
Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro
    1020                1025                1030

CCT GGC TTC GAC AGT GTC ATT GCC CGA GGC CAC ACC GAG CCT GAT CCG      1678
Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro
1035                1040                1045                1050
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ACC CAG GAC ACT GAG TTG GAG CTG GAT GGC CAG CAA GTG GTG GTG CCC      1726
Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro
                1055                1060                1065

CAG GGC CAG CCT GTG CCC TGC CCA GAG TTC AGC AGC TCC ACA TTC TCC      1774
Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser
            1070                1075                1080

CAG AGC GAG TAC CTC ATC TAC CAG GAG AGC CAG TGT CGC CTG CGC TAC      1822
Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr
        1085                1090                1095

CTG CTG GAG GTC CAC CTC TGA GTGCCCGCCC TGTCCCCCGG GGTCCTGCAA         1873
Leu Leu Glu Val His Leu  *
    1100                1105

GGCTGGACTG TGATCTTCAA TCATCCTGCC CATCTCTGGT ACCCCTATAT CACTCCTTTT    1933

TTTCAAGAAT ACAATACGTT GTTGTTAACT ATAGTCACCA TGCTGTACAA GATCCCTGAA    1993

CTTATGCCTC CTAACTGAAA TTTTGTATTC TTTGACACAT CTGCCCAGTC CCTCTCCTCC    2053

CAGCCCATGG TAACCAGCAT TTGACTCTTT ACTTGTATAA GGGCAGCTTT TATAGGTTCC    2113

ACATGTAAGT GAGATCATGC AGTGTTTGTC TTTCTGTGCC TGGCTTATTT CACTCAGCAT    2173

AATGTGCACC GGGTTCACCC ATGTTTTCAT AAATGACAAG ATTTCCTCCT TTAAAAAAAA    2233

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                                  2265
```

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 534 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu Lys
 1               5                  10                  15

Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
            20                  25                  30

Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg Val
        35                  40                  45

Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr Glu
    50                  55                  60

Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn Asn
65                  70                  75                  80

Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe Thr
                85                  90                  95

Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Ile
```

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            100                 105                 110

Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys Lys
        115                 120                 125

Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe Val
    130                 135                 140

Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp Glu
145                 150                 155                 160

Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr Val
                165                 170                 175

Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys Leu
            180                 185                 190

Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala Leu
        195                 200                 205

Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys Gln
    210                 215                 220

Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Leu
225                 230                 235                 240

Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser His
                245                 250                 255

Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro Pro
            260                 265                 270

Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu Val
        275                 280                 285

Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu Gln
    290                 295                 300

Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
305                 310                 315                 320

Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu Tyr
                325                 330                 335

Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys
            340                 345                 350

Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu Asp
        355                 360                 365

Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His
    370                 375                 380

Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
385                 390                 395                 400

Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
                405                 410                 415

Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys Gly
```

```
            420                 425                 430

Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg
        435                 440                 445

Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro
    450                 455                 460

Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr
465                 470                 475                 480

Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln
                485                 490                 495

Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln
            500                 505                 510

Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr Leu
        515                 520                 525

Leu Glu Val His Leu  *
    530
```

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:
(F) TISSUE TYPE: Uterus

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:221..1843
(D) OTHER INFORMATION:/product= "Poly ADP Ribose Polymerase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
TGGGACTGGT CGCCTGACTC GGCCTGCCCC AGCCTCTGCT TCACCCCACT GGTGGCCAAA      60

TAGCCGATGT CTAATCCCCC ACACAAGCTC ATCCCCGGCC TCTGGGATTG TTGGGAATTC     120

TCTCCCTAAT TCACGCCTGA GGCTCATGGA GAGTTGCTAG ACCTGGGACT GCCCTGGGAG     180

GCGCACACAA CCAGGCCGGG TGGCAGCCAG GACCTCTCCC ATG TCC CTG CTT TTC       235
                                              Met Ser Leu Leu Phe
                                              535

TTG GCC ATG GCT CCA AAG CCG AAG CCC TGG GTA CAG ACT GAG GGC CCT       283
```

```
Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro
540                 545                 550                 555

GAG AAG AAG AAG GGC CGG CAG GCA GGA AGG GAG GAG GAC CCC TTC CGC      331
Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg
                560                 565                 570

TCC ACC GCT GAG GCC CTC AAG GCC ATA CCC GCA GAG AAG CGC ATA ATC      379
Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile
            575                 580                 585

CGC GTG GAT CCA ACA TGT CCA CTC AGC AGC AAC CCC GGG ACC CAG GTG      427
Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val
        590                 595                 600

TAT GAG GAC TAC AAC TGC ACC CTG AAC CAG ACC AAC ATC GAG AAC AAC      475
Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn
    605                 610                 615

AAC AAC AAG TTC TAC ATC ATC CAG CTG CTC CAA GAC AGC AAC CGC TTC      523
Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe
620                 625                 630                 635

TTC ACC TGC TGG AAC CGC TGG GGC CGT GTG GGA GAG GTC GGC CAG TCA      571
Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser
                640                 645                 650

AAG ATC AAC CAC TTC ACA AGG CTA GAA GAT GCA AAG AAG GAC TTT GAG      619
Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu
            655                 660                 665

AAG AAA TTT CGG GAA AAG ACC AAG AAC AAC TGG GCA GAG CGG GAC CAC      667
Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His
        670                 675                 680

TTT GTG TCT CAC CCG GGC AAG TAC ACA CTT ATC GAA GTA CAG GCA GAG      715
Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu
    685                 690                 695

GAT GAG GCC CAG GAA GCT GTG GTG AAG GTG GAC AGA GGC CCA GTG AGG      763
Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg
700                 705                 710                 715

ACT GTG ACT AAG CGG GTG CAG CCC TGC TCC CTG GAC CCA GCC ACG CAG      811
Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln
                720                 725                 730

AAG CTC ATC ACT AAC ATC TTC AGC AAG GAG ATG TTC AAG AAC ACC ATG      859
Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met
            735                 740                 745

GCC CTC ATG GAC CTG GAT GTG AAG AAG ATG CCC CTG GGA AAG CTG AGC      907
Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser
        750                 755                 760

AAG CAA CAG ATT GCA CGG GGT TTC GAG GCC TTG GAG GCG CTG GAG GAG      955
Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
    765                 770                 775
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GCC CTG AAA GGC CCC ACG GAT GGT GGC CAA AGC CTG GAG GAG CTG TCC      1003
Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser
780                 785                 790                 795

TCA CAC TTT TAC ACC GTC ATC CCG CAC AAC TTC GGC CAC AGC CAG CCC      1051
Ser His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro
                800                 805                 810

CCG CCC ATC AAT TCC CCT GAG CTT CTG CAG GCC AAG AAG GAC ATG CTG      1099
Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu
            815                 820                 825

CTG GTG CTG GCG GAC ATC GAG CTG GCC CAG GCC CTG CAG GCA GTC TCT      1147
Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser
        830                 835                 840

GAG CAG GAG AAG ACG GTG GAG GAG GTG CCA CAC CCC CTG GAC CGA GAC      1195
Glu Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp
    845                 850                 855

TAC CAG CTT CTC AAG TGC CAG CTG CAG CTG CTA GAC TCT GGA GCA CCT      1243
Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro
860                 865                 870                 875

GAG TAC AAG GTG ATA CAG ACC TAC TTA GAA CAG ACT GGC AGC AAC CAC      1291
Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His
                880                 885                 890

AGG TGC CCT ACA CTT CAA CAC ATC TGG AAA GTA AAC CAA GAA GGG GAG      1339
Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu
            895                 900                 905

GAA GAC AGA TTC CAG GCC CAC TCC AAA CTG GGT AAT CGG AAG CTG CTG      1387
Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu
        910                 915                 920

TGG CAT GGC ACC AAC ATG GCC GTG GTG GCC GCC ATC CTC ACT AGT GGG      1435
Trp His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly
    925                 930                 935

CTC CGC ATC ATG CCA CAT TCT GGT GGG CGT GTT GGC AAG GGC ATC TAC      1483
Leu Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr
940                 945                 950                 955

TTT GCC TCA GAG AAC AGC AAG TCA GCT GGA TAT GTT ATT GGC ATG AAG      1531
Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys
                960                 965                 970

TGT GGG GCC CAC CAT GTC GGC TAC ATG TTC CTG GGT GAG GTG GCC CTG      1579
Cys Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu
            975                 980                 985

GGC AGA GAG CAC CAT ATC AAC ACG GAC AAC CCC AGC TTG AAG AGC CCA      1627
Gly Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro
        990                 995                1000

CCT CCT GGC TTC GAC AGT GTC ATT GCC CGA GGC CAC ACC GAG CCT GAT      1675
Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp
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    1005                1010                1015

CCG ACC CAG GAC ACT GAG TTG GAG CTG GAT GGC CAG CAA GTG GTG GTG      1723
Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val
1020                1025                1030                1035

CCC CAG GGC CAG CCT GTG CCC TGC CCA GAG TTC AGC AGC TCC ACA TTC      1771
Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe
                1040                1045                1050

TCC CAG AGC GAG TAC CTC ATC TAC CAG GAG AGC CAG TGT CGC CTG CGC      1819
Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg
            1055                1060                1065

TAC CTG CTG GAG GTC CAC CTC TGA GTGCCCGCCC TGTCCCCCGG GGTCCTGCAA      1873
Tyr Leu Leu Glu Val His Leu  *
        1070                1075

GGCTGGACTG TGATCTTCAA TCATCCTGCC CATCTCTGGT ACCCCTATAT CACTCCTTTT     1933

TTTCAAGAAT ACAATACGTT GTTGTTAACT ATAGTCACCA TGCTGTACAA GATCCCTGAA     1993

CTTATGCCTC CTAACTGAAA TTTTGTATTC TTTGACACAT CTGCCCAGTC CCTCTCCTCC     2053

CAGCCCATGG TAACCAGCAT TTGACTCTTT ACTTGTATAA GGGCAGCTTT TATAGGTTCC     2113

ACATGTAAGT GAGATCATGC AGTGTTTGTC TTTCTGTGCC TGGCTTATTT CACTCAGCAT     2173

AATGTGCACC GGGTTCACCC ATGTTTTCAT AAATGACAAG ATTTCCTCCT TTAAAAAAAA     2233

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                                   2265
```

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 541 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
Met Ser Leu Leu Phe Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val
  1               5                  10                  15

Gln Thr Glu Gly Pro Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu
            20                  25                  30

Glu Asp Pro Phe Arg Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala
        35                  40                  45

Glu Lys Arg Ile Ile Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn
    50                  55                  60

Pro Gly Thr Gln Val Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr
65                  70                  75                  80

Asn Ile Glu Asn Asn Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln
```

85 90 95

Asp Ser Asn Arg Phe Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly
100 105 110

Glu Val Gly Gln Ser Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala
115 120 125

Lys Lys Asp Phe Glu Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp
130 135 140

Ala Glu Arg Asp His Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile
145 150 155 160

Glu Val Gln Ala Glu Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp
165 170 175

Arg Gly Pro Val Arg Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu
180 185 190

Asp Pro Ala Thr Gln Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met
195 200 205

Phe Lys Asn Thr Met Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro
210 215 220

Leu Gly Lys Leu Ser Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu
225 230 235 240

Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser
245 250 255

Leu Glu Glu Leu Ser Ser His Phe Tyr Thr Val Ile Pro His Asn Phe
260 265 270

Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala
275 280 285

Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala
290 295 300

Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His
305 310 315 320

Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu
325 330 335

Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln
340 345 350

Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val
355 360 365

Asn Gln Glu Gly Glu Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly
370 375 380

Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala
385 390 395 400

Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val

```
                405                 410                 415

Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr
            420                 425                 430

Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu
        435                 440                 445

Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro
    450                 455                 460

Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly
465                 470                 475                 480

His Thr Glu Pro Asp Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly
                485                 490                 495

Gln Gln Val Val Val Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe
            500                 505                 510

Ser Ser Ser Thr Phe Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser
        515                 520                 525

Gln Cys Arg Leu Arg Tyr Leu Leu Glu Val His Leu  *
    530                 535                 540
```

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1740 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mus musculus

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:112..1710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
CCCGGCTTTC ACTTTTTCTG CTGCCTCGGG GAACACCTCG AGCCAACTGC TTCCTAACTC      60

AGGGTGGGCA GAACTGACGG GATCTAAGCT TCTGCATCTC TGAGGAGAAC C ATG GCT      117
                                                          Met Ala

CCA AAA CGA AAG GCC TCT GTG CAG ACT GAG GGC TCC AAG AAG CAG CGA      165
Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg
    545                 550                 555
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```
CAA GGG ACA GAG GAG GAG GAC AGC TTC CGG TCC ACT GCC GAG GCT CTC        213
Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu
560                 565                 570                 575

AGA GCA GCA CCT GCT GAT AAT CGG GTC ATC CGT GTG GAC CCC TCA TGT        261
Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys
                580                 585                 590

CCA TTC AGC CGG AAC CCC GGG ATA CAG GTC CAC GAG GAC TAT GAC TGT        309
Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys
            595                 600                 605

ACC CTG AAC CAG ACC AAC ATC GGC AAC AAC AAC AAC AAG TTC TAT ATT        357
Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe Tyr Ile
        610                 615                 620

ATC CAA CTG CTG GAG GAG GGT AGT CGC TTC TTC TGC TGG AAT CGC TGG        405
Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp
    625                 630                 635

GGC CGC GTG GGA GAG GTG GGC CAG AGC AAG ATG AAC CAC TTC ACC TGC        453
Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys
640                 645                 650                 655

CTG GAA GAT GCA AAG AAG GAC TTT AAG AAG AAA TTT TGG GAG AAG ACT        501
Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu Lys Thr
                660                 665                 670

AAA AAC AAA TGG GAG GAG CGG GAC CGT TTT GTG GCC CAG CCC AAC AAG        549
Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys
            675                 680                 685

TAC ACA CTT ATA GAA GTC CAG GGA GAA GCA GAG AGC CAA GAG GCT GTA        597
Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val
        690                 695                 700

GTG AAG GCC TTA TCT CCC CAG GTG GAC AGC GGC CCT GTG AGG ACC GTG        645
Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val
    705                 710                 715

GTC AAG CCC TGC TCC CTA GAC CCT GCC ACC CAG AAC CTT ATC ACC AAC        693
Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn
720                 725                 730                 735

ATC TTC AGC AAA GAG ATG TTC AAG AAC GCA ATG ACC CTC ATG AAC CTG        741
Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu
                740                 745                 750

GAT GTG AAG AAG ATG CCC TTG GGA AAG CTG ACC AAG CAG CAG ATT GCC        789
Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala
            755                 760                 765

CGT GGC TTC GAG GCC TTG GAA GCT CTA GAG GAG GCC ATG AAA AAC CCC        837
Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro
        770                 775                 780

ACA GGG GAT GGC CAG AGC CTG GAA GAG CTC TCC TCC TGC TTC TAC ACT        885
Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr
```

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    785                 790                 795

GTC ATC CCA CAC AAC TTC GGC CGC AGC CGA CCC CCG CCC ATC AAC TCC      933
Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser
800                 805                 810                 815

CCT GAT GTG CTT CAG GCC AAG AAG GAC ATG CTG CTG GTG CTA GCG GAC      981
Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp
                820                 825                 830

ATC GAG TTG GCG CAG ACC TTG CAG GCA GCC CCT GGG GAG GAG GAG GAG     1029
Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu
            835                 840                 845

AAA GTG GAA GAG GTG CCA CAC CCA CTG GAT CGA GAC TAC CAG CTC CTC     1077
Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu
        850                 855                 860

AGG TGC CAG CTT CAA CTG CTG GAC TCC GGG GAG TCC GAG TAC AAG GCA     1125
Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala
    865                 870                 875

ATA CAG ACC TAC CTG AAA CAG ACT GGC AAC AGC TAC AGG TGC CCA AAC     1173
Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn
880                 885                 890                 895

CTG CGG CAT GTT TGG AAA GTG AAC CGA GAA GGG GAG GGA GAC AGG TTC     1221
Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe
                900                 905                 910

CAG GCC CAC TCC AAA CTG GGC AAT CGG AGG CTG CTG TGG CAC GGC ACC     1269
Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr
            915                 920                 925

AAT GTG GCC GTG GTG GCT GCC ATC CTC ACC AGT GGG CTC CGA ATC ATG     1317
Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met
        930                 935                 940

CCA CAC TCG GGT GGT CGT GTT GGC AAG GGT ATT TAT TTT GCC TCT GAG     1365
Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu
    945                 950                 955

AAC AGC AAG TCA GCT GGC TAT GTT ACC ACC ATG CAC TGT GGG GGC CAC     1413
Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His
960                 965                 970                 975

CAG GTG GGC TAC ATG TTC CTG GGC GAG GTG GCC CTC GGC AAA GAG CAC     1461
Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His
                980                 985                 990

CAC ATC ACC ATC GAT GAC CCC AGC TTG AAG AGT CCA CCC CCT GGC TTT     1509
His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe
            995                 1000                1005

GAC AGC GTC ATC GCC CGA GGC CAA ACC GAG CCG GAT CCC GCC CAG GAC     1557
Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp
        1010                1015                1020

ATT GAA CTT GAA CTG GAT GGG CAG CCG GTG GTG GTG CCC CAA GGC CCG     1605
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```
Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro
    1025                1030                1035

CCT GTG CAG TGC CCG TCA TTC AAA AGC TCC AGC TTC AGC CAG AGT GAA      1653
Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu
1040                1045                1050                1055

TAC CTC ATA TAC AAG GAG AGC CAG TGT CGC CTG CGC TAC CTG CTG GAG      1701
Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu
                1060                1065                1070

ATT CAC CTC TAAGCTGCTT GCCCTCCCTA GGTCCAAGCC                        1740
Ile His Leu
```

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```
Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys
 1               5                  10                  15

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
            20                  25                  30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
        35                  40                  45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
    50                  55                  60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
65                  70                  75                  80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
                85                  90                  95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
            100                 105                 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
        115                 120                 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
    130                 135                 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
145                 150                 155                 160

Ala Val Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg
                165                 170                 175

Thr Val Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile
```

180 185 190

Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met
195 200 205

Asn Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln
210 215 220

Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys
225 230 235 240

Asn Pro Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe
245 250 255

Tyr Thr Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile
260 265 270

Asn Ser Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu
275 280 285

Ala Asp Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu
290 295 300

Glu Glu Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
305 310 315 320

Leu Leu Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr
325 330 335

Lys Ala Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys
340 345 350

Pro Asn Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp
355 360 365

Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His
370 375 380

Gly Thr Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
385 390 395 400

Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
405 410 415

Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly
420 425 430

Gly His Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys
435 440 445

Glu His His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro
450 455 460

Gly Phe Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala
465 470 475 480

Gln Asp Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln
485 490 495

Gly Pro Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln

```
           500                 505                 510

Ser Glu Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu
       515                 520                 525

Leu Glu Ile His Leu
    530
```

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mus musculus

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..1584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
ATG GCT CCA AAA CGA AAG GCC TCT GTG CAG ACT GAG GGC TCC AAG AAG        48
Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys
    535                 540                 545

CAG CGA CAA GGG ACA GAG GAG GAG GAC AGC TTC CGG TCC ACT GCC GAG        96
Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
550                 555                 560                 565

GCT CTC AGA GCA GCA CCT GCT GAT AAT CGG GTC ATC CGT GTG GAC CCC       144
Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
                570                 575                 580

TCA TGT CCA TTC AGC CGG AAC CCC GGG ATA CAG GTC CAC GAG GAC TAT       192
Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
            585                 590                 595

GAC TGT ACC CTG AAC CAG ACC AAC ATC GGC AAC AAC AAC AAC AAG TTC       240
Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
        600                 605                 610

TAT ATT ATC CAA CTG CTG GAG GAG GGT AGT CGC TTC TTC TGC TGG AAT       288
Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
    615                 620                 625

CGC TGG GGC CGC GTG GGA GAG GTG GGC CAG AGC AAG ATG AAC CAC TTC       336
Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
630                 635                 640                 645
```

```
ACC TGC CTG GAA GAT GCA AAG AAG GAC TTT AAG AAG AAA TTT TGG GAG          384
Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
                650                 655                 660

AAG ACT AAA AAC AAA TGG GAG GAG CGG GAC CGT TTT GTG GCC CAG CCC          432
Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
            665                 670                 675

AAC AAG TAC ACA CTT ATA GAA GTC CAG GGA GAA GCA GAG AGC CAA GAG          480
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
        680                 685                 690

GCT GTA GTG AAG GTG GAC AGC GGC CCT GTG AGG ACC GTG GTC AAG CCC          528
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro
    695                 700                 705

TGC TCC CTA GAC CCT GCC ACC CAG AAC CTT ATC ACC AAC ATC TTC AGC          576
Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser
710                 715                 720                 725

AAA GAG ATG TTC AAG AAC GCA ATG ACC CTC ATG AAC CTG GAT GTG AAG          624
Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys
                730                 735                 740

AAG ATG CCC TTG GGA AAG CTG ACC AAG CAG CAG ATT GCC CGT GGC TTC          672
Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe
            745                 750                 755

GAG GCC TTG GAA GCT CTA GAG GAG GCC ATG AAA AAC CCC ACA GGG GAT          720
Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp
        760                 765                 770

GGC CAG AGC CTG GAA GAG CTC TCC TCC TGC TTC TAC ACT GTC ATC CCA          768
Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro
    775                 780                 785

CAC AAC TTC GGC CGC AGC CGA CCC CCG CCC ATC AAC TCC CCT GAT GTG          816
His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val
790                 795                 800                 805

CTT CAG GCC AAG AAG GAC ATG CTG CTG GTG CTA GCG GAC ATC GAG TTG          864
Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu
                810                 815                 820

GCG CAG ACC TTG CAG GCA GCC CCT GGG GAG GAG GAG GAG AAA GTG GAA          912
Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu Lys Val Glu
            825                 830                 835

GAG GTG CCA CAC CCA CTG GAT CGA GAC TAC CAG CTC CTC AGG TGC CAG          960
Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln
        840                 845                 850

CTT CAA CTG CTG GAC TCC GGG GAG TCC GAG TAC AAG GCA ATA CAG ACC         1008
Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr
    855                 860                 865

TAC CTG AAA CAG ACT GGC AAC AGC TAC AGG TGC CCA AAC CTG CGG CAT         1056
Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His
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870                 875                 880                 885

GTT TGG AAA GTG AAC CGA GAA GGG GAG GGA GAC AGG TTC CAG GCC CAC      1104
Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His
                890                 895                 900

TCC AAA CTG GGC AAT CGG AGG CTG CTG TGG CAC GGC ACC AAT GTG GCC      1152
Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala
            905                 910                 915

GTG GTG GCT GCC ATC CTC ACC AGT GGG CTC CGA ATC ATG CCA CAC TCG      1200
Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser
        920                 925                 930

GGT GGT CGT GTT GGC AAG GGT ATT TAT TTT GCC TCT GAG AAC AGC AAG      1248
Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys
    935                 940                 945

TCA GCT GGC TAT GTT ACC ACC ATG CAC TGT GGG GGC CAC CAG GTG GGC      1296
Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly
950                 955                 960                 965

TAC ATG TTC CTG GGC GAG GTG GCC CTC GGC AAA GAG CAC CAC ATC ACC      1344
Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr
                970                 975                 980

ATC GAT GAC CCC AGC TTG AAG AGT CCA CCC CCT GGC TTT GAC AGC GTC      1392
Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val
            985                 990                 995

ATC GCC CGA GGC CAA ACC GAG CCG GAT CCC GCC CAG GAC ATT GAA CTT      1440
Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu
        1000                1005                1010

GAA CTG GAT GGG CAG CCG GTG GTG GTG CCC CAA GGC CCG CCT GTG CAG      1488
Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
    1015                1020                1025

TGC CCG TCA TTC AAA AGC TCC AGC TTC AGC CAG AGT GAA TAC CTC ATA      1536
Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
1030                1035                1040                1045

TAC AAG GAG AGC CAG TGT CGC CTG CGC TAC CTG CTG GAG ATT CAC CTC      1584
Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
                1050                1055                1060

TAA                                                                 1587
```

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys

```
1               5                  10                  15
Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
            20                  25                  30
Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
        35                  40                  45
Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
    50                  55                  60
Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
65                  70                  75                  80
Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
                85                  90                  95
Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
            100                 105                 110
Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
        115                 120                 125
Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
    130                 135                 140
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
145                 150                 155                 160
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro
                165                 170                 175
Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser
            180                 185                 190
Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys
        195                 200                 205
Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe
    210                 215                 220
Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp
225                 230                 235                 240
Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro
                245                 250                 255
His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val
            260                 265                 270
Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu
        275                 280                 285
Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu Lys Val Glu
    290                 295                 300
Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln
305                 310                 315                 320
Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr
```

```
                325                 330                 335

Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His
            340                 345                 350

Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His
        355                 360                 365

Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala
    370                 375                 380

Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser
385                 390                 395                 400

Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys
                405                 410                 415

Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly
            420                 425                 430

Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr
        435                 440                 445

Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val
    450                 455                 460

Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu
465                 470                 475                 480

Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
                485                 490                 495

Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
            500                 505                 510

Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
        515                 520                 525
```

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:2
(D) OTHER INFORMATION:/note= "Xaa steht fuer 1 bis 5 andere Aminosaeuren"

(ix) FEATURE:

(A) NAME/KEY: Region
(B) LOCATION:3
(D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Pro Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly Ile Tyr Phe Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:1
(D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:6
(D) OTHER INFORMATION:/note= "Xaa steht fuer Ile oder Val"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:9
(D) OTHER INFORMATION:/note= "Xaa steht fuer 1 bis 5 andere Aminosaeuren"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:10
(D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Gly Xaa Xaa Xaa Gly Lys
1 5 10 15

Gly Ile Tyr Phe Ala
20

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:16
(D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:21
(D) OTHER INFORMATION:/note= "Xaa steht fuer Ile oder Val"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:24
(D) OTHER INFORMATION:/note= "Xaa steht fuer 1 bis 5 andere Aminosaeuren"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:25
(D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:6
(D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```
Leu Leu Trp His Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Leu Xaa
1               5                  10                  15

Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly
            20                  25                  30

Ile Tyr Phe Ala Xaa Xaa Xaa Ser Lys Ser Ala Xaa Tyr
        35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:1
(D) OTHER INFORMATION:/note= "Xaa steht fuer Leu oder Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu
20

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:21
(D) OTHER INFORMATION:/note= "Xaa steht fuer Asp oder Glu"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:22
(D) OTHER INFORMATION:/note= "Xaa steht fuer 10 oder 11 andere Aminosaeuren"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Tyr Xaa Xaa
1 5 10 15

Gln Leu Leu Xaa Xaa Xaa Trp Gly Arg Val Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```
Ala Xaa Xaa Xaa Phe Xaa Lys Xaa Xaa Xaa Xaa Lys Thr Xaa Asn Xaa
1               5                   10                  15

Trp Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Pro Xaa Lys
            20                  25
```

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:4
(D) OTHER INFORMATION:/note= "Xaa steht fuer Ile oder Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```
Gln Xaa Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15

Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Leu Gly Lys Leu
            20                  25                  30

Xaa Xaa Xaa Gln Ile Xaa Xaa Xaa Xaa Xaa Xaa Leu
        35                  40
```

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Phe Tyr Thr Xaa Ile Pro His Xaa Phe Gly Xaa Xaa Xaa Pro Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Lys Xaa Xaa Xaa Leu Xaa Xaa Leu Xaa Asp Ile Glu Xaa Ala Xaa Xaa
1 5 10 15

Leu

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Gly Xaa Xaa Xaa Leu Xaa Glu Val Ala Leu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

(A) NAME/KEY: Region
(B) LOCATION:14
(D) OTHER INFORMATION:/note= "Xaa steht fuer 7 bis 9 andere Aminosaeuren"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Gly Xaa Xaa Ser Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Leu Xaa
1 5 10 15

Gly Xaa Xaa Val
20

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:2
(D) OTHER INFORMATION:/note= "Xaa steht fuer Tyr oder Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Glu Xaa Xaa Xaa Tyr Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Tyr Leu Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala
1 5 10 15

Leu Asn Glu Ser

20

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Lys Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg
1 5 10 15

Asn Leu His Cys
20

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Cys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
1 5 10 15

Ala Glu Ala Leu Lys
20

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu
1 5 10 15

Glu Ala Leu Lys
20

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
1 5 10 15

Ala Leu Lys

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
1 5 10 15

Ala Met Lys

We claim:

1. A poly(ADP-ribose) polymerase (PARP) homolog derived from a human or non-human mammal which has an amino acid sequence which has
   a) a functional NAD^+ binding domain
      and
   b) no zinc finger sequence motif of the general formula

$$CX_2CX_mHX_2C$$

   in which
   m is an integral value from 28 or 30, and the X radicals are, independently of one another, any amino acid.

2. A PARP homolog as claimed in claim 1, wherein the functional NAD^+ binding domain comprises one of the following general sequence motifs:

$PX_n(S/T)GX_3GKGIYFA$,
$(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFA$ or
$LLWHG(S/T)X_7IL(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFAX_3SKSAXY$

   in which
   n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid.

3. A PARP homolog as claimed in either of the preceding claims, comprising at least another one of the following part-sequence motifs:

$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$,
$AX_3FXKX_4KTXNXWX_5FX_3PXK$,
$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$,
$FYTXIPHXFGX_3PP$; and
$KX_3LX_2LXDIEXAX_2L$,

   in which the X radicals are, independently of one another, any amino acid.

4. A PARP homolog as claimed in any of the preceding claims, selected from human PARP homologs, which has the amino acid sequence shown in SEQ ID NO: 2 (human PARP2) or SEQ ID NO: 4 or 6 (human PARP3 type 1 or 2); or murine PARP homologs which

have the amino acid sequence shown in SEQ ID NO:8 (mouse PARP long form) or SEQ ID No:10 (mouse PARP short form).

5. A binding partner having specifity for PARP homologs as claimed in any of the preceding claims, selected from
   a) antibodies and fragments thereof,
   b) protein-like compounds which interact with a part-sequence of the protein, and
   c) low molecular weight effectors which modulate the catalytic PARP activity or another biological function of a PARP molecule.

6. A nucleic acid comprising
   a) a nucleotide sequence coding for at least one PARP homolog as claimed in any of claims 1 to 4, or the complementary nucleotide sequence thereof;
   b) a nucleotide sequence which hybridizes with a sequence as specified in a) under stringent conditions; or
   c) nucleotide sequences which are derived from the nucleotide sequences defined in a) and b) through the degeneracy of the genetic code.

7. A nucleic acid as claimed in claim 6, comprising

   a) nucleotides +3 to +1715 shown in SEQ ID NO:1;
   b) nucleotides +242 to +1843 shown in SEQ ID NO:3;
   c) nucleotides +221 to +1843 shown in SEQ ID NO:5;
   d) nucleotides +112 to +1710 shown in SEQ ID NO:7; or
   e) nucleotides +1 to +1584 shown in SEQ ID NO:9.

8. An expression cassette comprising, under the genetic control of at least one regulatory nucleotide sequence, at least one nucleotide sequence as claimed in either of claims 6 and 7.

9. A recombinant vector comprising at least one expression cassette as claimed in claim 8.

10. A recombinant microorganism comprising at least one recombinant vector as claimed in claim 9.

11. A transgenic mammal comprising a vector as claimed in claim 9.

12. A PARP-deficient mammal or PARP-deficient eukaryotic cell, in which functional expression of at least one gene which codes for a PARP homolog as claimed in any of claims 1 to 4 is inhibited.

13. An in vitro detection method for PARP inhibitors, which comprises

a) incubating an unsupported or supported polyADP-ribosylatable target with a reaction mixture comprising
   a1) a PARP homolog as claimed in any of claims 1 to 4,
   a2) a PARP activator; and
   a3) a PARP inhibitor or an analyte in which at least one PARP inhibitor is suspected;
b) carrying out the polyADP ribosylation reaction; and
c) determining the polyADP ribosylation of the target qualitatively or quantitatively.

14. A method as claimed in claim 13, wherein the PARP homolog is preincubated with the PARP activator and the PARP inhibitor or an analyte in which at least one PARP inhibitor is suspected, before the polyADP ribosylation reaction is carried out.

15. A method as claimed in either of claims 13 and 14, wherein the polyADP-ribosylatable target is a histone protein.

16. A method as claimed in any of claims 13 to 15, wherein the PARP activator is activated DNA.

17. A method as claimed in any of claims 13 to 16, wherein the polyADP ribosylation reaction is started by adding NAD^+.

18. A method as claimed in any of claims 13 to 17, wherein the polyADP ribosylation of the supported target is determined using anti-poly(ADP-ribose) antibodies.

19. A method as claimed in any of claims 13 to 17, wherein the unsupported target is labeled with an acceptor fluorophore.

20. A method as claimed in claim 19, wherein the polyADP ribosylation of the unsupported target is determined using anti-poly(ADP-ribose) antibody which is labeled with a donor fluorophore which is able to transfer energy to the acceptor fluorophore.

21. A method as claimed in either of claims 19 and 20, wherein the target is biotinylated histone, and the acceptor fluorophore is coupled thereto via avidin or streptavidin.

22. A method as claimed in either of claims 20 and 21, wherein the anti-poly(ADP-ribose) antibody carries a europium cryptate as donor fluorophore.

23. An in vitro screening method for binding partners for a PARP molecule, which comprises

a1) immobilizing at least one PARP homolog as claimed in any of claims 1 to 4 on a support;

b1) contacting the immobilized PARP homolog with an analyte in which at least one binding partner is suspected; and

c1) determining, where appropriate after an incubation period, analyte constituents bound to the immobilized PARP homolog;

or

a2) immobilizing on a support an analyte which comprises at least one possible binding partner for a PARP molecule;

b2) contacting the immobilized analyte with at least one PARP homolog as claimed in any of claims 1 to 4 for which a binding partner is sought; and

c2) examining the immobilized analyte, where appropriate after an incubation period, for binding of the PARP homolog.

24. A method for the qualitative or quantitative determination of nucleic acids encoding a PARP homolog as claimed in any of claims 1 to 4, which comprises

a) incubating a biological sample with a defined amount of an exogenous nucleic acid as claimed in either of claims 6 and 7, hybridizing under stringent conditions, determining the hybridizing nucleic acids and, where appropriate, comparing with a standard; or

b) incubating a biological sample with a pair of oligonucleotide primers with specificity for a PARP homolog-encoding nucleic acid, amplifying the nucleic acid, determining the amplification product and, where appropriate, comparing with a standard.

25. A method for the qualitative or quantitative determination of a PARP homolog as claimed in any of claims 1 to 4, which comprises

a) incubating a biological sample with a binding partner specific for a PARP homolog,
b) detecting the binding partner/PARP complex and, where appropriate,
c) comparing the result with a standard.

26. A method as claimed in claim 25, wherein the binding partner is an antibody or a binding fragment thereof, which carries a detectable label where appropriate.

27. A method as claimed in any of claims 24 to 26 for diagnosing energy deficit-mediated illnesses.

28. A method for determining the efficacy of PARP effectors, which comprises
a) incubating a PARP homolog as claimed in any of claims 1 to 4 with an analyte which comprises an effector of a physiological or pathological PARP activity; removing the effector again where appropriate; and
b) determining the activity of the PARP homolog, where appropriate after adding substrates or cosubstrates.

29. A gene therapy composition, which comprises in a vehicle acceptable for gene therapy a nucleic acid construct which
a) comprises an antisense nucleic acid against a coding nucleic acid as claimed in either of claims 6 and 7; or
b) a ribozyme against a nucleic acid as claimed in either of claims 6 and 7; or
c) codes for a specific PARP inhibitor.

30. A pharmaceutical composition comprising, in a pharmaceutically acceptable vehicle, at least one PARP protein as claimed in any of claims 1 to 4, at least one PARP binding partner as claimed in claim 5 or at least one coding nucleotide sequence as claimed in claim 6 or 7.

31. The use of low molecular weight PARP binding partners as claimed in claim 5 for the manufacture of a pharmaceutical agent for the diagnosis or therapy of pathological states in the development and/or progress of which at least one PARP protein, or a polypeptide derived therefrom, is involved.

32. The use of low molecular weight PARP binding partners as claimed in claim 5 for the manufacture of a pharmaceutical agent for the diagnosis or therapy of pathological states mediated by an energy deficit.

Abstract

The invention relates to poly(ADP-ribose)polymerase (PARP) homologs which have an amino acid sequence which has

a) a functional NAD^+ binding domain
and
b) no zinc finger sequence motif of the general formula

$$CX_2CX_mHX_2C$$

in which
m is an integral value from 28 or 30, and the X radicals are, independently of one another, any amino acid;

and the functional equivalents thereof; nucleic acids coding therefor; antibodies with specificity for the novel protein; pharmaceutical and gene therapy compositions which comprise products according to the invention; methods for the analytical determination of the proteins and nucleic acids according to the invention; methods for identifying effectors or binding partners of the proteins according to the invention; novel PARP effectors; and methods for determining the activity of such effectors.

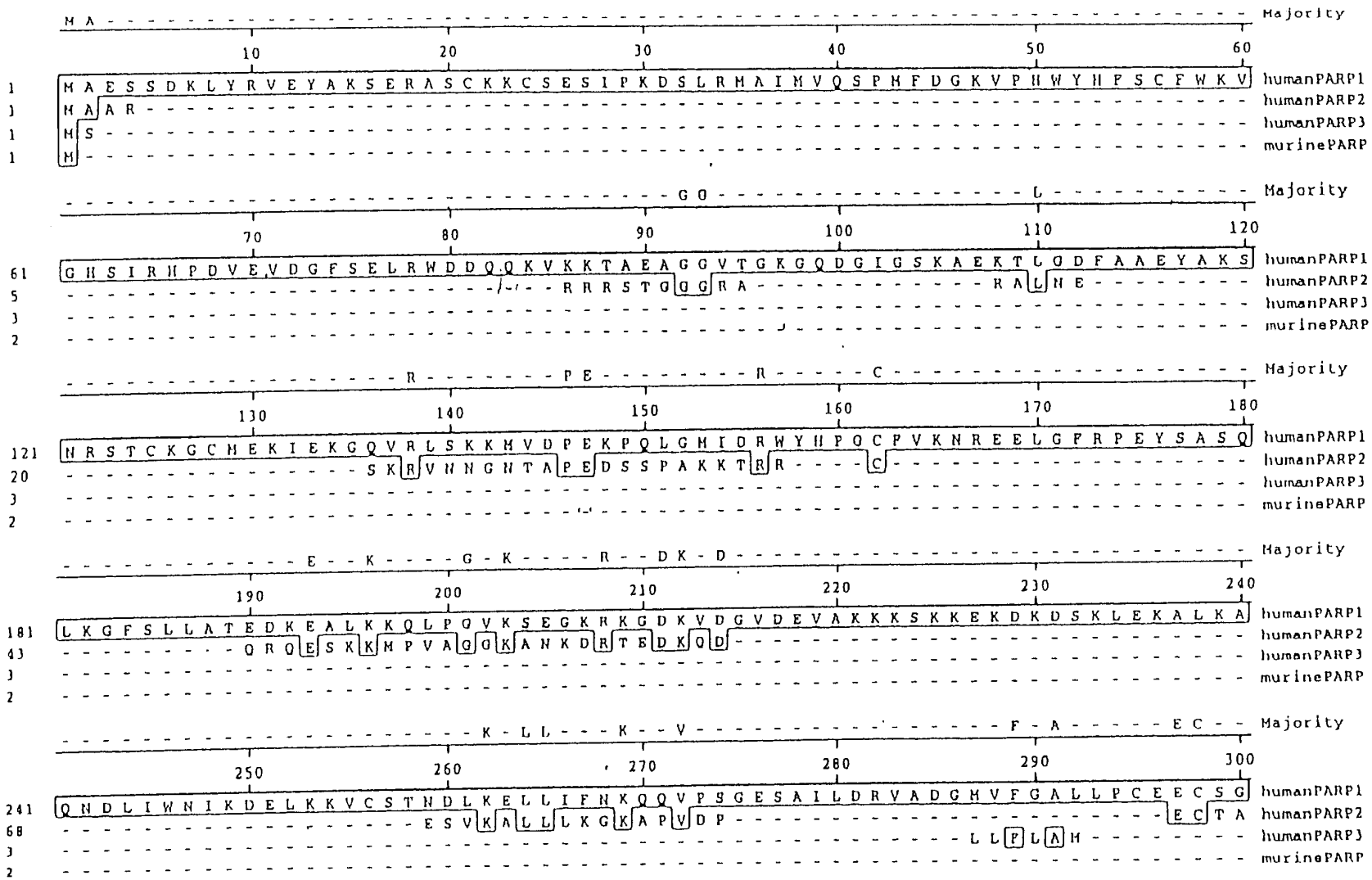
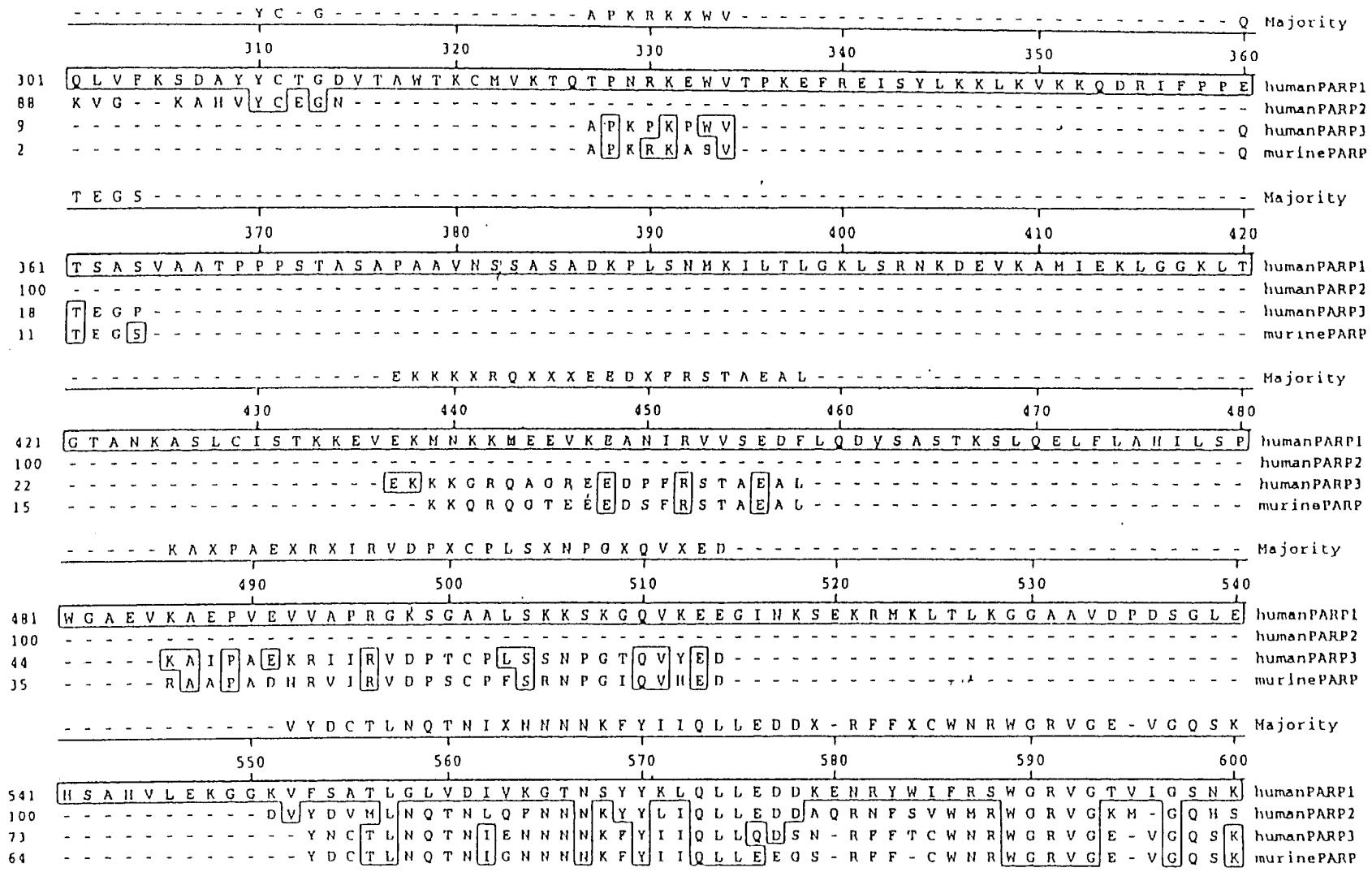


Fig. 1(1)



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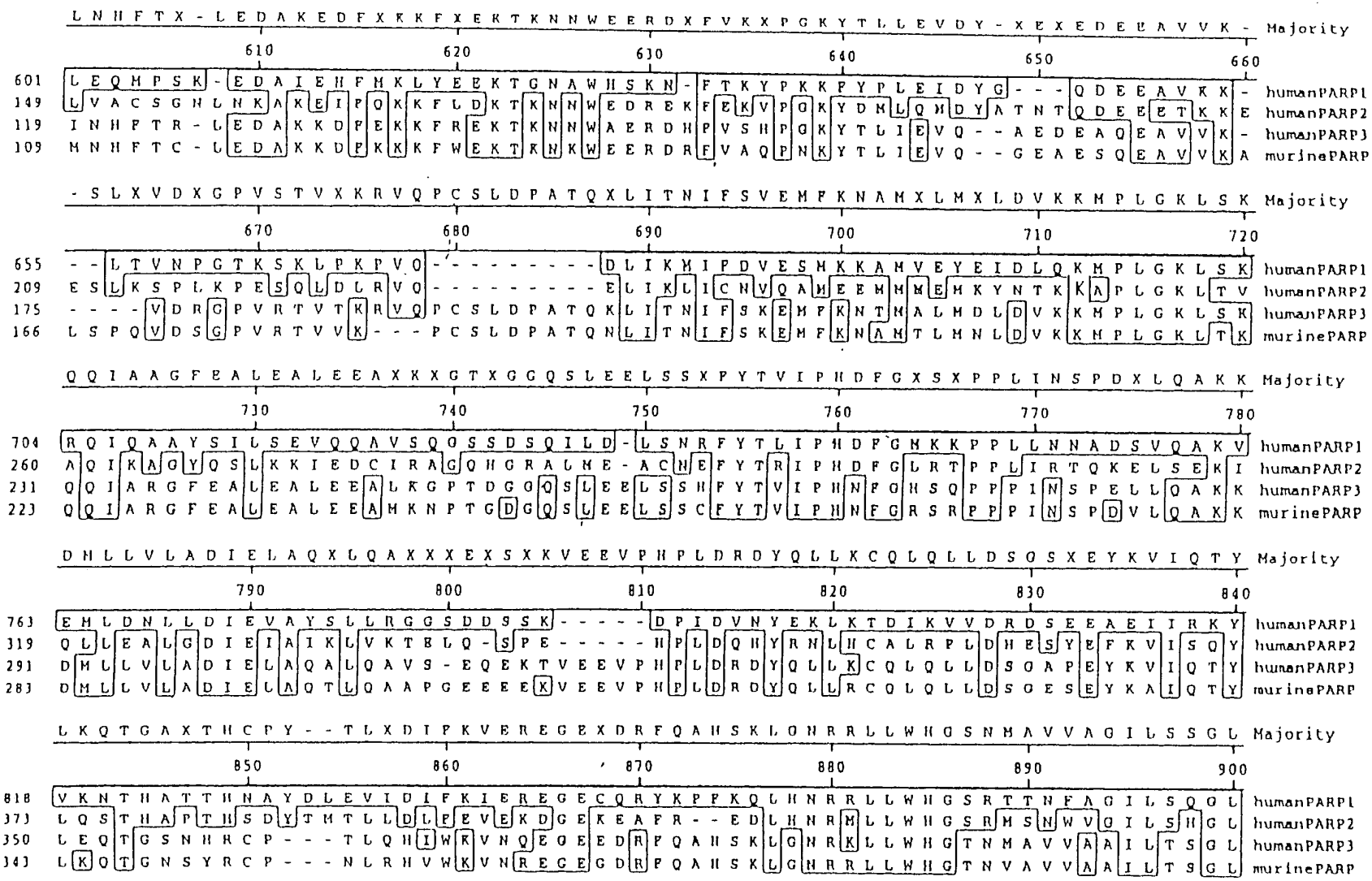
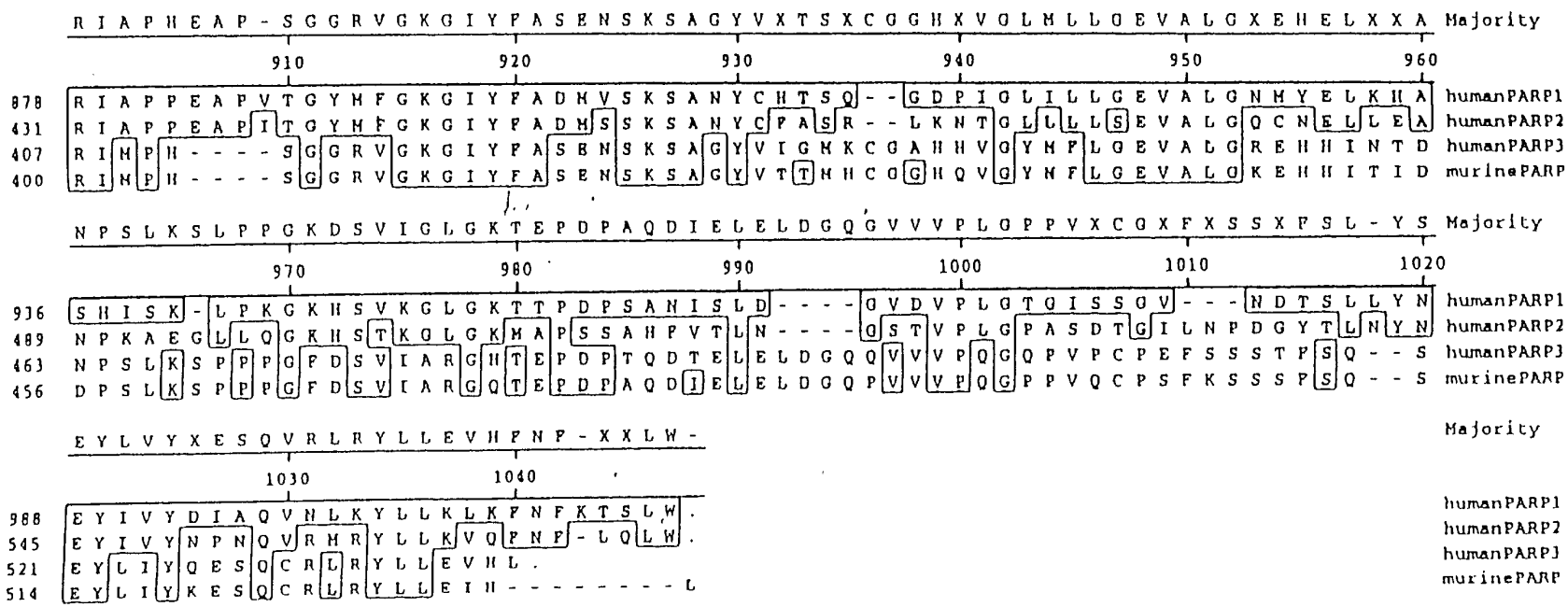


Fig. 1(3)

09/701586



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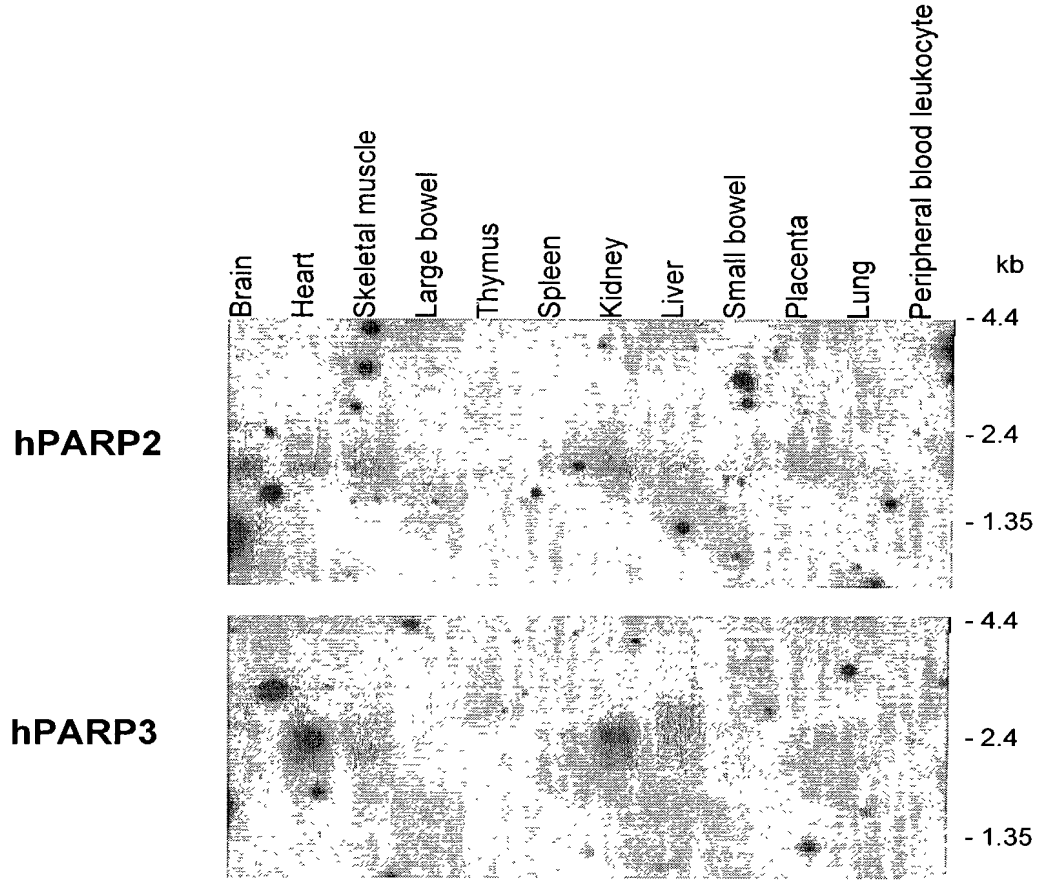
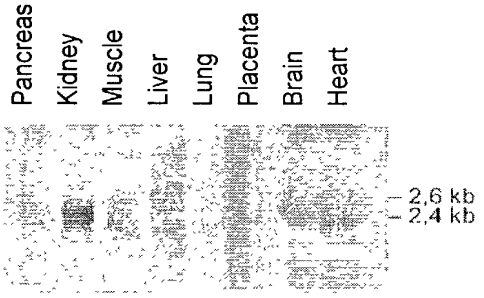
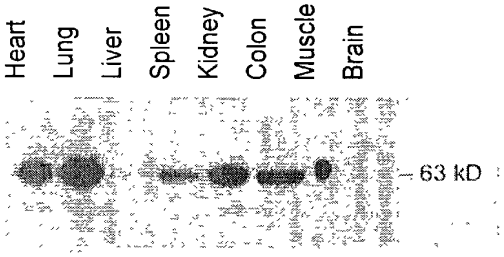


Fig. 2



Northern Blot Analysis
Human PARP3 Tissue Distribution

Fig. 3



Western Blot Analysis
PARP3 Tissue Distribution

Fig. 4

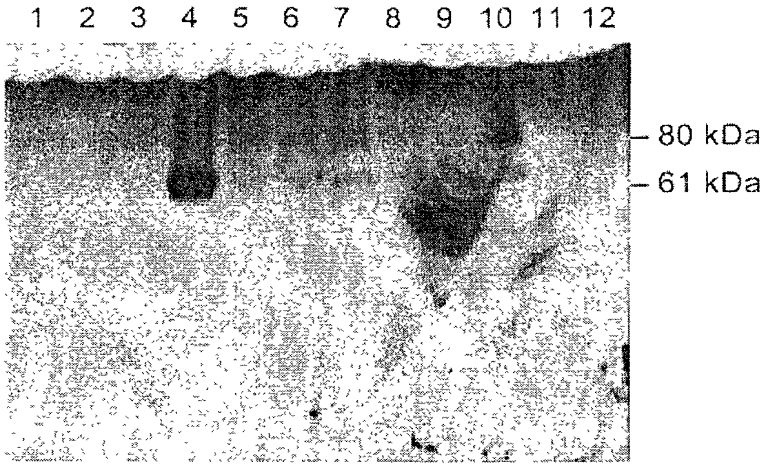
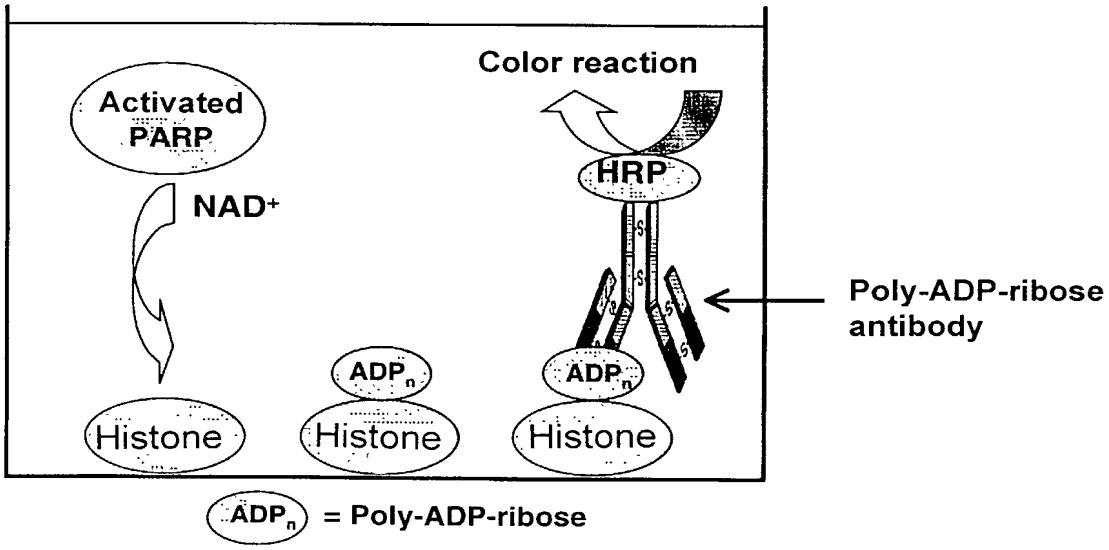


Fig. 5



HRP = Horseradish-Peroxidase

Fig. 6

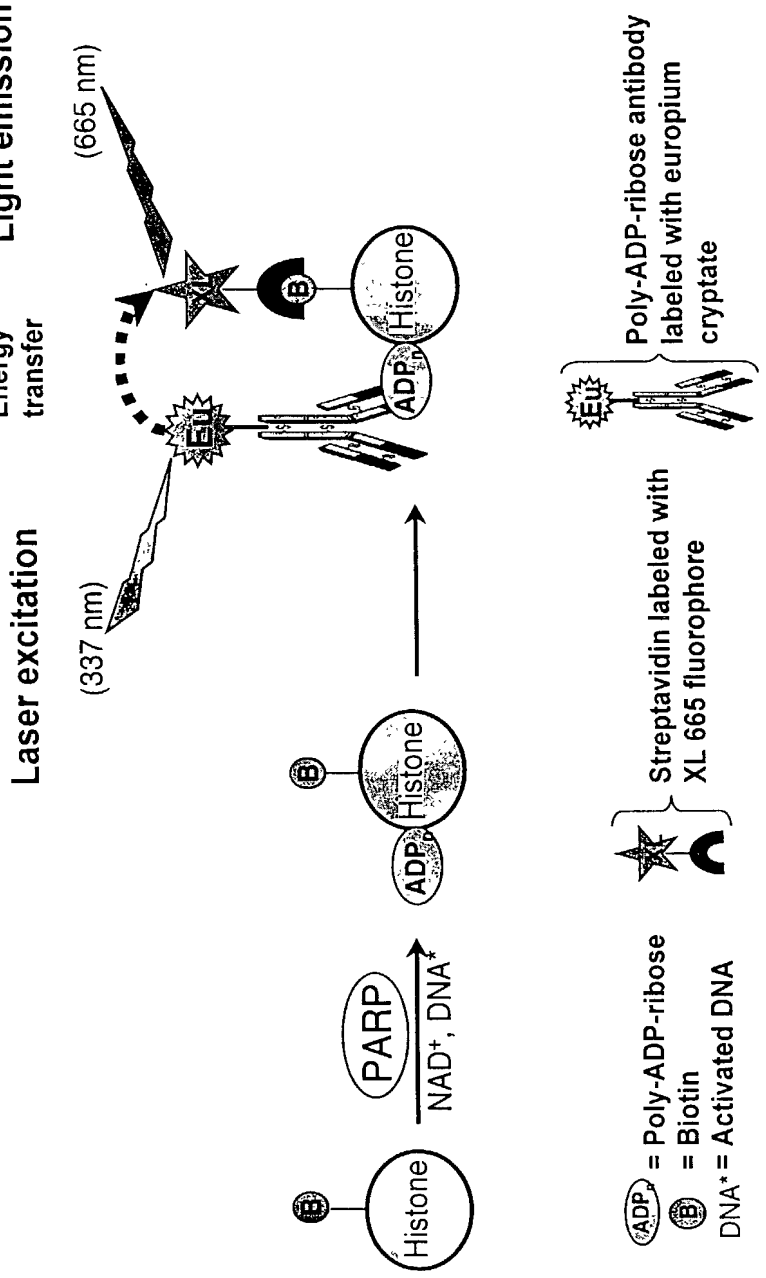

Laser excitation
Energy transfer
Light emission
(337 nm)
(665 nm)
Eu
XL
B
Histone
ADP
PARP
NAD+, DNA*
Streptavidin labeled with XL 665 fluorophore
Poly-ADP-ribose antibody labeled with europium cryptate
= Poly-ADP-ribose
= Biotin
DNA* = Activated DNA

Fig. 7

(9)

Declaration, Power of Attorney

0050/049100

We (I), the undersigned inventor(s), hereby declare(s) that:

My residence, post office address and citizenship are as stated below next to my name,

We (I) believe that we are (I am) the original, first, and joint (sole) inventor(s) of the subject matter which is claimed and for which a patent is sought on the invention entitled

Poly(ADP-ribose)polymerase-gene

the specification of which

[✓] is attached hereto.

[ ] was filed on _____ as

Application Serial No. _____

and amended on _____.

[x] was filed as PCT international application

Number PCT/EP 99/ 03889

on June 4, 1999

and was amended under PCT Article 19

on _____ (if applicable).

We (I) hereby state that we (I) have reviewed and understand the contents of the above–identified specification, including the claims, as amended by any amendment referred to above.

We (I) acknowledge the duty to disclose information known to be material to the patentability of this application as defined in Section 1.56 of Title 37 Code of Federal Regulations.

We (I) hereby claim foreign priority benefits under 35 U.S.C. § 119(a)–(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed. Prior Foreign Application(s)

Application No.	**Country**	**Day/Month/Year**	**Priority Claimed**	
19825213.7	*Germany*	*05 June 1998*	[x] Yes	[ ] No
19908837.3	*Germany*	*01 March 1999*	[x] Yes	[ ] No

We (I) hereby claim the benefit under Title 35, United States Codes, § 119(e) of any United States provisional application(s) listed below.

(Application Number)	(Filing Date)
(Application Number)	(Filing Date)

We (I) hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s), or § 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR § 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

Application Serial No.	**Filing Date**	**Status (pending, patented, abandoned)**

And we (I) hereby appoint **Messrs. HERBERT. B. KEIL**, Registration Number 18,967; and **RUSSEL E. WEINKAUF**, Registration Number 18,495; the address of both being Messrs. Keil & Weinkauf, 1101 Connecticut Ave., N.W., Washington, D.C. 20036 (telephone 202–659–0100), our attorneys, with full power of substitution and revocation, to prosecute this application, to make alterations and amendments therein, to sign the drawings, to receive the patent, and to transact all business in the Patent Office connected therewith.

We (I) declare that all statements made herein of our (my) own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

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<110> Kock, Michael
Hoeger, Thomas
Kroeger, Burkhard
Otterbach, Bernd
Lubisch, Wilfried
Lemaire, Hans-Georg

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Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp Tyr
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Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
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    305                 310                 315

cag ctt ctc aag tgc cag ctg cag ctg cta gac tct gga gca cct gag     1246
Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu
320                 325                 330                 335

tac aag gtg ata cag acc tac tta gaa cag act ggc agc aac cac agg     1294
Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg
                340                 345                 350

tgc cct aca ctt caa cac atc tgg aaa gta aac caa gaa ggg gag gaa     1342
Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu
            355                 360                 365

gac aga ttc cag gcc cac tcc aaa ctg ggt aat cgg aag ctg ctg tgg     1390
Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp
        370                 375                 380

cat ggc acc aac atg gcc gtg gtg gcc gcc atc ctc act agt ggg ctc     1438
```

```
His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu
    385                 390                 395

cgc atc atg cca cat tct ggt ggg cgt gtt ggc aag ggc atc tac ttt      1486
Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe
400                 405                 410                 415

gcc tca gag aac agc aag tca gct gga tat gtt att ggc atg aag tgt      1534
Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys
                420                 425                 430

ggg gcc cac cat gtc ggc tac atg ttc ctg ggt gag gtg gcc ctg ggc      1582
Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly
            435                 440                 445

aga gag cac cat atc aac acg gac aac ccc agc ttg aag agc cca cct      1630
Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro
        450                 455                 460

cct ggc ttc gac agt gtc att gcc cga ggc cac acc gag cct gat ccg      1678
Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro
    465                 470                 475

acc cag gac act gag ttg gag ctg gat ggc cag caa gtg gtg gtg ccc      1726
Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro
480                 485                 490                 495

cag ggc cag cct gtg ccc tgc cca gag ttc agc agc tcc aca ttc tcc      1774
Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser
                500                 505                 510

cag agc gag tac ctc atc tac cag gag agc cag tgt cgc ctg cgc tac      1822
Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr
            515                 520                 525

ctg ctg gag gtc cac ctc tga gtgcccgccc tgtcccccgg ggtcctgcaa         1873
Leu Leu Glu Val His Leu
        530

ggctggactg tgatcttcaa tcatcctgcc catctctggt acccctatat cactcctttt    1933

tttcaagaat acaatacgtt gttgttaact atagtcacca tgctgtacaa gatccctgaa    1993

cttatgcctc ctaactgaaa ttttgtattc tttgacacat ctgcccagtc cctctcctcc    2053

cagcccatgg taaccagcat ttgactcttt acttgtataa gggcagcttt tataggttcc    2113

acatgtaagt gagatcatgc agtgtttgtc tttctgtgcc tggcttattt cactcagcat    2173

aatgtgcacc gggttcaccc atgttttcat aaatgacaag atttcctcct ttaaaaaaaa    2233

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa                                  2265
```

<210> 4
<211> 533
<212> PRT
<213> Homo sapiens

<400> 4

```
Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu Lys
 1               5                  10                  15

Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
            20                  25                  30

Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg Val
        35                  40                  45

Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr Glu
    50                  55                  60

Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn Asn
65                  70                  75                  80

Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe Thr
                85                  90                  95

Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Ile
            100                 105                 110

Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys Lys
        115                 120                 125

Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe Val
    130                 135                 140

Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp Glu
145                 150                 155                 160

Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr Val
                165                 170                 175

Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys Leu
            180                 185                 190

Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala Leu
        195                 200                 205

Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys Gln
    210                 215                 220

Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Leu
225                 230                 235                 240

Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser His
                245                 250                 255

Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro Pro
            260                 265                 270

Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu Val
        275                 280                 285

Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu Gln
    290                 295                 300
```

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Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
305                 310                 315                 320

Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu Tyr
                325                 330                 335

Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys
            340                 345                 350

Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu Asp
        355                 360                 365

Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His
    370                 375                 380

Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
385                 390                 395                 400

Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
                405                 410                 415

Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys Gly
            420                 425                 430

Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg
        435                 440                 445

Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro
    450                 455                 460

Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr
465                 470                 475                 480

Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln
                485                 490                 495

Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln
            500                 505                 510

Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr Leu
        515                 520                 525

Leu Glu Val His Leu
    530
```

<210> 5
<211> 2265
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (221)...(1843)
<223> product is Poly ADP Ribose Polymerase; from uterus tissue

<400> 5

tgggactggt cgcctgactc ggcctgcccc agcctctgct tcaccccact ggtggccaaa 60

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tagccgatgt ctaatccccc acacaagctc atccccggcc tctgggattg ttgggaattc      120

tctccctaat tcacgcctga ggctcatgga gagttgctag acctgggact gccctgggag      180

gcgcacacaa ccaggccggg tggcagccag gacctctccc atg tcc ctg ctt ttc        235
                                             Met Ser Leu Leu Phe
                                               1               5

ttg gcc atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct        283
Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro
                 10                  15                  20

gag aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc        331
Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg
             25                  30                  35

tcc acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc        379
Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile
         40                  45                  50

cgc gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg        427
Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val
     55                  60                  65

tat gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac        475
Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn
 70                  75                  80                  85

aac aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc        523
Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe
                 90                  95                 100

ttc acc tgc tgg aac cgc tgg ggc cgt gtg gga gag gtc ggc cag tca        571
Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser
             105                 110                 115

aag atc aac cac ttc aca agg cta gaa gat gca aag aag gac ttt gag        619
Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu
         120                 125                 130

aag aaa ttt cgg gaa aag acc aag aac aac tgg gca gag cgg gac cac        667
Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His
     135                 140                 145

ttt gtg tct cac ccg ggc aag tac aca ctt atc gaa gta cag gca gag        715
Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu
150                 155                 160                 165

gat gag gcc cag gaa gct gtg gtg aag gtg gac aga ggc cca gtg agg        763
Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg
                 170                 175                 180

act gtg act aag cgg gtg cag ccc tgc tcc ctg gac cca gcc acg cag        811
Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln
             185                 190                 195

aag ctc atc act aac atc ttc agc aag gag atg ttc aag aac acc atg        859
Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met
         200                 205                 210
```

```
gcc ctc atg gac ctg gat gtg aag aag atg ccc ctg gga aag ctg agc       907
Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser
    215                 220                 225

aag caa cag att gca cgg ggt ttc gag gcc ttg gag gcg ctg gag gag       955
Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
230                 235                 240                 245

gcc ctg aaa ggc ccc acg gat ggt ggc caa agc ctg gag gag ctg tcc      1003
Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser
                250                 255                 260

tca cac ttt tac acc gtc atc ccg cac aac ttc ggc cac agc cag ccc      1051
Ser His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro
            265                 270                 275

ccg ccc atc aat tcc cct gag ctt ctg cag gcc aag aag gac atg ctg      1099
Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu
        280                 285                 290

ctg gtg ctg gcg gac atc gag ctg gcc cag gcc ctg cag gca gtc tct      1147
Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser
    295                 300                 305

gag cag gag aag acg gtg gag gag gtg cca cac ccc ctg gac cga gac      1195
Glu Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp
310                 315                 320                 325

tac cag ctt ctc aag tgc cag ctg cag ctg cta gac tct gga gca cct      1243
Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro
                330                 335                 340

gag tac aag gtg ata cag acc tac tta gaa cag act ggc agc aac cac      1291
Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His
            345                 350                 355

agg tgc cct aca ctt caa cac atc tgg aaa gta aac caa gaa ggg gag      1339
Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu
        360                 365                 370

gaa gac aga ttc cag gcc cac tcc aaa ctg ggt aat cgg aag ctg ctg      1387
Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu
    375                 380                 385

tgg cat ggc acc aac atg gcc gtg gtg gcc gcc atc ctc act agt ggg      1435
Trp His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly
390                 395                 400                 405

ctc cgc atc atg cca cat tct ggt ggg cgt gtt ggc aag ggc atc tac      1483
Leu Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr
                410                 415                 420

ttt gcc tca gag aac agc aag tca gct gga tat gtt att ggc atg aag      1531
Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys
            425                 430                 435

tgt ggg gcc cac cat gtc ggc tac atg ttc ctg ggt gag gtg gcc ctg      1579
Cys Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu
        440                 445                 450
```

```
ggc aga gag cac cat atc aac acg gac aac ccc agc ttg aag agc cca      1627
Gly Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro
    455                 460                 465

cct cct ggc ttc gac agt gtc att gcc cga ggc cac acc gag cct gat      1675
Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp
470                 475                 480                 485

ccg acc cag gac act gag ttg gag ctg gat ggc cag caa gtg gtg gtg      1723
Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val
                490                 495                 500

ccc cag ggc cag cct gtg ccc tgc cca gag ttc agc agc tcc aca ttc      1771
Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe
            505                 510                 515

tcc cag agc gag tac ctc atc tac cag gag agc cag tgt cgc ctg cgc      1819
Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg
        520                 525                 530

tac ctg ctg gag gtc cac ctc tga gtgcccgccc tgtcccccgg ggtcctgcaa      1873
Tyr Leu Leu Glu Val His Leu
    535                 540

ggctggactg tgatcttcaa tcatcctgcc catctctggt acccctatat cactcctttt      1933

tttcaagaat acaatacgtt gttgttaact atagtcacca tgctgtacaa gatccctgaa      1993

cttatgcctc ctaactgaaa ttttgtattc tttgacacat ctgcccagtc cctctcctcc      2053

cagcccatgg taaccagcat ttgactcttt acttgtataa gggcagcttt tataggttcc      2113

acatgtaagt gagatcatgc agtgtttgtc tttctgtgcc tggcttattt cactcagcat      2173

aatgtgcacc gggttcaccc atgttttcat aaatgacaag atttcctcct ttaaaaaaaa      2233

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa                                    2265
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<210> 6
<211> 540
<212> PRT
<213> Homo sapiens

<400> 6

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Met Ser Leu Leu Phe Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val
  1               5                  10                  15

Gln Thr Glu Gly Pro Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu
             20                  25                  30

Glu Asp Pro Phe Arg Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala
         35                  40                  45

Glu Lys Arg Ile Ile Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn
     50                  55                  60

Pro Gly Thr Gln Val Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr
```

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 65                  70                  75                  80

Asn Ile Glu Asn Asn Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln
                85                  90                  95

Asp Ser Asn Arg Phe Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly
            100                 105                 110

Glu Val Gly Gln Ser Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala
        115                 120                 125

Lys Lys Asp Phe Glu Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp
    130                 135                 140

Ala Glu Arg Asp His Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile
145                 150                 155                 160

Glu Val Gln Ala Glu Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp
                165                 170                 175

Arg Gly Pro Val Arg Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu
            180                 185                 190

Asp Pro Ala Thr Gln Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met
        195                 200                 205

Phe Lys Asn Thr Met Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro
    210                 215                 220

Leu Gly Lys Leu Ser Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu
225                 230                 235                 240

Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser
                245                 250                 255

Leu Glu Glu Leu Ser Ser His Phe Tyr Thr Val Ile Pro His Asn Phe
            260                 265                 270

Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala
        275                 280                 285

Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala
    290                 295                 300

Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His
305                 310                 315                 320

Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu
                325                 330                 335

Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln
            340                 345                 350

Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val
        355                 360                 365

Asn Gln Glu Gly Glu Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly
    370                 375                 380
```

```
Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala
385                 390                 395                 400

Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val
                405                 410                 415

Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr
            420                 425                 430

Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu
        435                 440                 445

Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro
    450                 455                 460

Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly
465                 470                 475                 480

His Thr Glu Pro Asp Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly
                485                 490                 495

Gln Gln Val Val Val Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe
            500                 505                 510

Ser Ser Ser Thr Phe Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser
        515                 520                 525

Gln Cys Arg Leu Arg Tyr Leu Leu Glu Val His Leu
    530                 535                 540


<210> 7
<211> 1740
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (112)...(1710)

<400> 7

cccggctttc acttttctg ctgcctcggg gaacacctcg agccaactgc ttcctaactc      60

agggtgggca gaactgacgg gatctaagct tctgcatctc tgaggagaac c atg gct      117
                                                          Met Ala
                                                            1

cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag cag cga      165
Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg
          5                  10                  15

caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag gct ctc      213
Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu
     20                  25                  30

aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc tca tgt      261
Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys
 35                  40                  45                  50
```

```
cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat gac tgt       309
Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys
                55                  60                  65

acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc tat att       357
Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe Tyr Ile
            70                  75                  80

atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat cgc tgg       405
Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp
        85                  90                  95

ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc acc tgc       453
Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys
    100                 105                 110

ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag aag act       501
Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu Lys Thr
115                 120                 125                 130

aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc aac aag       549
Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys
                135                 140                 145

tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag gct gta       597
Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val
            150                 155                 160

gtg aag gcc tta tct ccc cag gtg gac agc ggc cct gtg agg acc gtg       645
Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val
        165                 170                 175

gtc aag ccc tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac       693
Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn
    180                 185                 190

atc ttc agc aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg       741
Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu
195                 200                 205                 210

gat gtg aag aag atg ccc ttg gga aag ctg acc aag cag cag att gcc       789
Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala
                215                 220                 225

cgt ggc ttc gag gcc ttg gaa gct cta gag gag gcc atg aaa aac ccc       837
Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro
            230                 235                 240

aca ggg gat ggc cag agc ctg gaa gag ctc tcc tcc tgc ttc tac act       885
Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr
        245                 250                 255

gtc atc cca cac aac ttc ggc cgc agc cga ccc ccg ccc atc aac tcc       933
Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser
    260                 265                 270

cct gat gtg ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac       981
Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp
275                 280                 285                 290
```

```
atc gag ttg gcg cag acc ttg cag gca gcc cct ggg gag gag gag gag      1029
Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu
                295                 300                 305

aaa gtg gaa gag gtg cca cac cca ctg gat cga gac tac cag ctc ctc      1077
Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu
            310                 315                 320

agg tgc cag ctt caa ctg ctg gac tcc ggg gag tcc gag tac aag gca      1125
Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala
        325                 330                 335

ata cag acc tac ctg aaa cag act ggc aac agc tac agg tgc cca aac      1173
Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn
    340                 345                 350

ctg cgg cat gtt tgg aaa gtg aac cga gaa ggg gag gga gac agg ttc      1221
Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe
355                 360                 365                 370

cag gcc cac tcc aaa ctg ggc aat cgg agg ctg ctg tgg cac ggc acc      1269
Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr
                375                 380                 385

aat gtg gcc gtg gtg gct gcc atc ctc acc agt ggg ctc cga atc atg      1317
Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met
            390                 395                 400

cca cac tcg ggt ggt cgt gtt ggc aag ggt att tat ttt gcc tct gag      1365
Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu
        405                 410                 415

aac agc aag tca gct ggc tat gtt acc acc atg cac tgt ggg ggc cac      1413
Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His
    420                 425                 430

cag gtg ggc tac atg ttc ctg ggc gag gtg gcc ctc ggc aaa gag cac      1461
Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His
435                 440                 445                 450

cac atc acc atc gat gac ccc agc ttg aag agt cca ccc cct ggc ttt      1509
His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe
                455                 460                 465

gac agc gtc atc gcc cga ggc caa acc gag ccg gat ccc gcc cag gac      1557
Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp
            470                 475                 480

att gaa ctt gaa ctg gat ggg cag ccg gtg gtg gtg ccc caa ggc ccg      1605
Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro
        485                 490                 495

cct gtg cag tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa      1653
Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu
    500                 505                 510

tac ctc ata tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag      1701
Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu
515                 520                 525                 530
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att cac ctc taagctgctt gccctcccta ggtccaagcc 1740
Ile His Leu

<210> 8
<211> 533
<212> PRT
<213> Mus musculus

<400> 8

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys
1 5 10 15

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
20 25 30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
35 40 45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
50 55 60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
65 70 75 80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
85 90 95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
100 105 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
115 120 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
130 135 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
145 150 155 160

Ala Val Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg
165 170 175

Thr Val Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile
180 185 190

Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met
195 200 205

Asn Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln
210 215 220

Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys
225 230 235 240

Asn Pro Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe
245 250 255

Tyr Thr Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile
260 265 270

Asn Ser Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu
275 280 285

Ala Asp Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu
290 295 300

Glu Glu Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
305 310 315 320

Leu Leu Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr
325 330 335

Lys Ala Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys
340 345 350

Pro Asn Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp
355 360 365

Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His
370 375 380

Gly Thr Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
385 390 395 400

Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
405 410 415

Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly
420 425 430

Gly His Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys
435 440 445

Glu His His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro
450 455 460

Gly Phe Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala
465 470 475 480

Gln Asp Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln
485 490 495

Gly Pro Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln
500 505 510

Ser Glu Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu
515 520 525

Leu Glu Ile His Leu
530

<210> 9
<211> 1587
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(1584)

<400> 9

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atg gct cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag        48
Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys
  1               5                  10                  15

cag cga caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag        96
Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
             20                  25                  30

gct ctc aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc       144
Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
         35                  40                  45

tca tgt cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat       192
Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
     50                  55                  60

gac tgt acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc       240
Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
 65                  70                  75                  80

tat att atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat       288
Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
                 85                  90                  95

cgc tgg ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc       336
Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
            100                 105                 110

acc tgc ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag       384
Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
        115                 120                 125

aag act aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc       432
Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
    130                 135                 140

aac aag tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag       480
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
145                 150                 155                 160

gct gta gtg aag gtg gac agc ggc cct gtg agg acc gtg gtc aag ccc       528
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro
                165                 170                 175

tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac atc ttc agc       576
Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser
            180                 185                 190

aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg gat gtg aag       624
Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys
        195                 200                 205

aag atg ccc ttg gga aag ctg acc aag cag cag att gcc cgt ggc ttc       672
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Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe
    210                 215                 220

gag gcc ttg gaa gct cta gag gag gcc atg aaa aac ccc aca ggg gat      720
Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp
225                 230                 235                 240

ggc cag agc ctg gaa gag ctc tcc tcc tgc ttc tac act gtc atc cca      768
Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro
                245                 250                 255

cac aac ttc ggc cgc agc cga ccc ccg ccc atc aac tcc cct gat gtg      816
His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val
            260                 265                 270

ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac atc gag ttg      864
Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu
        275                 280                 285

gcg cag acc ttg cag gca gcc cct ggg gag gag gag gag aaa gtg gaa      912
Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu Lys Val Glu
    290                 295                 300

gag gtg cca cac cca ctg gat cga gac tac cag ctc ctc agg tgc cag      960
Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln
305                 310                 315                 320

ctt caa ctg ctg gac tcc ggg gag tcc gag tac aag gca ata cag acc     1008
Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr
                325                 330                 335

tac ctg aaa cag act ggc aac agc tac agg tgc cca aac ctg cgg cat     1056
Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His
            340                 345                 350

gtt tgg aaa gtg aac cga gaa ggg gag gga gac agg ttc cag gcc cac     1104
Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His
        355                 360                 365

tcc aaa ctg ggc aat cgg agg ctg ctg tgg cac ggc acc aat gtg gcc     1152
Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala
    370                 375                 380

gtg gtg gct gcc atc ctc acc agt ggg ctc cga atc atg cca cac tcg     1200
Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser
385                 390                 395                 400

ggt ggt cgt gtt ggc aag ggt att tat ttt gcc tct gag aac agc aag     1248
Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys
                405                 410                 415

tca gct ggc tat gtt acc acc atg cac tgt ggg ggc cac cag gtg ggc     1296
Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly
            420                 425                 430

tac atg ttc ctg ggc gag gtg gcc ctc ggc aaa gag cac cac atc acc     1344
Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr
        435                 440                 445
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atc gat gac ccc agc ttg aag agt cca ccc cct ggc ttt gac agc gtc      1392
Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val
    450                 455                 460

atc gcc cga ggc caa acc gag ccg gat ccc gcc cag gac att gaa ctt      1440
Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu
465                 470                 475                 480

gaa ctg gat ggg cag ccg gtg gtg gtg ccc caa ggc ccg cct gtg cag      1488
Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
                485                 490                 495

tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa tac ctc ata      1536
Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
            500                 505                 510

tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag att cac ctc      1584
Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
        515                 520                 525

taa                                                                  1587
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<210> 10
<211> 528
<212> PRT
<213> Mus musculus

<400> 10

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Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys
  1               5                  10                  15

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
             20                  25                  30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
         35                  40                  45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
     50                  55                  60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
 65                  70                  75                  80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
                 85                  90                  95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
            100                 105                 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
        115                 120                 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
    130                 135                 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
145                 150                 155                 160
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```
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro
                  165                 170                 175

Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser
            180                 185                 190

Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys
        195                 200                 205

Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe
    210                 215                 220

Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp
225                 230                 235                 240

Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro
                245                 250                 255

His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val
            260                 265                 270

Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu
        275                 280                 285

Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu Lys Val Glu
    290                 295                 300

Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln
305                 310                 315                 320

Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr
                325                 330                 335

Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His
            340                 345                 350

Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His
        355                 360                 365

Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala
    370                 375                 380

Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser
385                 390                 395                 400

Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys
                405                 410                 415

Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly
            420                 425                 430

Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr
        435                 440                 445

Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val
    450                 455                 460

Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu
465                 470                 475                 480
```

```
Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
                485                 490                 495

Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
            500                 505                 510

Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
        515                 520                 525


<210> 11
<211> 18
<212> PRT
<213> artificial sequence

<220>
<223> NAD+ binding domain

<220>
<221> VARIANT
<222> (2)...(6), (9)...(11)
<223> any amino acid; residues 3 to 6 may be present or absent

<220>
<221> VARIANT
<222> (7)
<223> amino acid residue 7 is either Ser or Thr

<400> 11

Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly Ile Tyr
  1               5                  10                  15

Phe Ala


<210> 12
<211> 25
<212> PRT
<213> artificial sequence

<220>
<223> NAD+ binding domain

<220>
<221> VARIANT
<222> (1), (14)
<223> amino acid residues 1 and 14 are either Ser or Thr

<220>
<221> VARIANT
<222> (2), (7), (9)...(13), (16)...(18)
<223> may be any amino acid; 10-13 may be present or absent

<220>
<221> VARIANT
<222> (6)
<223> amino acid residue 6 is either Ile or Val
```

<400> 12

Xaa Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa
1 5 10 15

Xaa Xaa Gly Lys Gly Ile Tyr Phe Ala
20 25

<210> 13
<211> 49
<212> PRT
<213> artificial sequence

<220>
<223> NAD+ binding domain

<220>
<221> VARIANT
<222> (6), (16), (29)
<223> Ser or Thr

<220>
<221> VARIANT
<222> (7)...(13), (17), (22), (24)...(28), (31)...(33), (41)...(43), (48)
<223> may be any amino acid; residues 25-28 may be present or absent

<220>
<221> VARIANT
<222> 21
<223> Ile or Val

<400> 13

Leu Leu Trp His Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Leu Xaa
1 5 10 15

Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
20 25 30

Xaa Gly Lys Gly Ile Tyr Phe Ala Xaa Xaa Xaa Ser Lys Ser Ala Xaa
35 40 45

Tyr

<210> 14
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> leucine zipper motif

<220>
<221> VARIANT
<222> (1)
<223> Leu or Val

<220>
<221> VARIANT
<222> (2)...(7), (9)...(14), (16)...(21)
<223> may be any amino acid

<400> 14

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu
20

<210> 15
<211> 37
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 1

<220>
<221> VARIANT
<222> (21)
<223> Asp or Glu

<220>
<221> VARIANT
<222> (2)...(10), (12)...(13), (15)...(16), (20), (22)...(32)
<223> may be any amino acid; residue 32 may be present or absent

<400> 15

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Tyr Xaa Xaa
1 5 10 15

Gln Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Trp Gly Arg Val Gly
35

<210> 16
<211> 29
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 2

<220>
<221> VARIANT
<222> (2)...(4), (6), (8)...(11), (14), (16), (18)...(22), (24)...(26), (28)
<223> may be any amino acid

<400> 16

Ala Xaa Xaa Xaa Phe Xaa Lys Xaa Xaa Xaa Xaa Lys Thr Xaa Asn Xaa
1 5 10 15

Trp Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Pro Xaa Lys
20 25

<210> 17
<211> 44
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 3

<220>
<221> VARIANT
<222> (2), (5)...(6), (8)...(16), (18)...(27), (33)...(35), (38)...(43)
<223> may be any amino acid

<220>
<221> VARIANT
<222> (4)
<223> Ile or Leu

<400> 17

Gln Xaa Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Leu Gly Lys Leu
20 25 30

Xaa Xaa Xaa Gln Ile Xaa Xaa Xaa Xaa Xaa Xaa Leu
35 40

<210> 18
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 4

<220>
<221> VARIANT
<222> (4), (8), (11)...(13)
<223> may be any amino acid

<400> 18

Phe Tyr Thr Xaa Ile Pro His Xaa Phe Gly Xaa Xaa Xaa Pro Pro
1 5 10 15

<210> 19
<211> 17
<212> PRT

<213> artificial sequence

<220>
<223> part-sequence motif 5

<220>
<221> VARIANT
<222> (2)...(4), (6)...(7), (9), (13), (15)...(16)
<223> may be any amino acid

<400> 19

Lys Xaa Xaa Xaa Leu Xaa Xaa Leu Xaa Asp Ile Glu Xaa Ala Xaa Xaa
1 5 10 15

Leu

<210> 20
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 6

<220>
<221> VARIANT
<222> (2)...(4), (6)
<223> may be any amino acid

<400> 20

Gly Xaa Xaa Xaa Leu Xaa Glu Val Ala Leu Gly
1 5 10

<210> 21
<211> 28
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 7

<220>
<221> VARIANT
<222> (2)...(3), (5)...(8), (10)...(12), (14)...(22), (24), (26)...(27)
<223> may be any amino acid; residues 21 and 22 may be present or absent

<400> 21

Gly Xaa Xaa Ser Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Gly Xaa Xaa Val
20 25

<210> 22
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 8

<220>
<221> VARIANT
<222> (2)
<223> Tyr or Phe

<220>
<221> VARIANT
<222> (3)...(4), (6)...(8), (10)...(13)
<223> may be any amino acid

<400> 22

Glu Xaa Xaa Xaa Tyr Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Tyr Leu Leu
1 5 10 15

<210> 23
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence for antibody production

<400> 23

Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala
1 5 10 15

Leu Asn Glu Ser
20

<210> 24
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence for antibody production

<400> 24

Lys Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg
1 5 10 15

Asn Leu His Cys
20

<210> 25
<211> 21
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence for antibody production

<400> 25

Cys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
1 5 10 15

Ala Glu Ala Leu Lys
20

<210> 26
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence for antibody production

<400> 26

Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu
1 5 10 15

Glu Ala Leu Lys
20

<210> 27
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence for antibody production

<400> 27

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
1 5 10 15

Ala Leu Lys

<210> 28
<211> 19
<212> PRT
<213> Mus musculus

<400> 28

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
1 5 10 15

Ala Met Lys

<210> 29
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> NAD+ binding domain

<220>
<221> VARIANT
<222> (2)...(4)
<223> may be any amino acid residue

<400> 29

Gly Xaa Xaa Xaa Gly Lys Gly
1 5

<210> 30
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> PARP zinc finger sequence motif

<220>
<221> VARIANT
<222> (2)...(3), (5)...(34), (36)...(37)
<223> may be any amino acid; residues 33 and 34 may be present or absent

<400> 30

Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa His Xaa Xaa Cys
35

<210> 31
<211> 10
<212> PRT
<213> Arabidopsis thaliana

<400> 31

Ala Ala Val Leu Asp Gln Trp Ile Pro Asp
1 5 10

<210> 32

<211> 39
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(39)

<400> 32

gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg 39
Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
1 5 10

<210> 33
<211> 13
<212> PRT
<213> Homo sapiens

<400> 33

Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
1 5 10